

# FIGURE 1

ACTGCACCTCGGTTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGCCGCAGGACCTGGAGCTCCGGCTCGCTTCCCG  
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCGCTGGGCTCCTGCCGCTTGCTG  
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCAGGTGCCGGGGCT  
GGTGGACAAGTTAACCAAGGGATGGTGACACCGCAAAGAAGAACTTGGCGGGAAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCAGCGAGATTCGCCTGCTGGAGATC  
CTGGAGGGCTGTGCAGAGCAGCGACTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA  
GGGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATTGACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCAGCGAGTGTGAAGTGGCTGGTGCT  
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAACCTGTGAGGAAAAACG  
AAAAGTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTTCGAAGAACG  
GAAGATGCCTGTGTGCCGCCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGGAAGACCTGTAATGTGCCGGACTTACCCTTAAATTATTCAAGGATGTCC  
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTGCAGTGGACAGCGGCCGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTTCTTA  
AACAGACTTGTATATTGATACTACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAACG  
TTGGCCGCATGGCCAACCTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA  
TCACAAATTTCACAAATAAGCATTTCAGCTGCTAGTTGTGGTTGTCCAAACTC  
ATCAATGTATCTTATCATGTCTGGATGGAAATTAACTCGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGAAAGAACCAAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCSDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGSLTNRDCGECEVGVLDE  
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## **FIGURE 3**

CAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCAC CGCGTCCGCCAGGCCAGGGAGGCGACGCGCCCAGCCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGCAGGAGGAGGCCCTTC  
CCTGCCGCCGCGCTCGGCTCTGGAGCATCCTCTGTGCCTGCTGGCACTGCGGGCGGAGGC  
CGGGCGCCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA  
TAGGATTTGAAGAAGATATCCTGATTGTT CAGAGGGAAAATGGCACCTTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATT CCTGTCCTGCGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAACAGTGCCCTCACAAGGCA  
TCAGTTGTTCAAGTTGGTTCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT  
TCTTAAAACATGTCAACAAGCTGAGTGCCAGGGCGGCTGCGAAATGGAGGCTTTGTAAT  
GAAAGACGCATCTGCAGTGCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCCACGATGTATGAATGGTGGACTTTGTGACTCCTGGTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACTGTGACAAAGCAAAC TGCTCAACCACCTGCTTTAATGGAGGGACC  
TGTTCTACCCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACAACCGTCAATGGAGGTAAATGCATTGGAAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGCTGCGAGCCTGGCTGGTGACAT  
GGAACCTGCCATGAACCCAACAAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCGGCCAGCTCAGGCAGC  
ACACGCCCTCACTTAAAAGGCCAGGGAGCGGGGATCCACCTGAATCCAATTACATCTGG  
**TGA**ACTCCGACATCTGAAACGTTAAGTTACACCAAGTTACAGCCTTGTAAACCTTCA  
TGTGTTGAATGTTCAAATAATGTTCATTACACTTAAGAATACTGGCCTGAATTTATTAGCT  
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTCTTGTTCAGTGTGAGTTGGCAGATATTTCAAATTACAATGCATTATGGT  
TCAGGTTAAAATTTCACTGAGCTGATTTAGTTGGCAGATATTTCAAATTACAATGCATTATGGT  
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAATCGTAAGTCACAAGAAT  
TTGGATGGTGAGTTAATGTTGAAGTTACAGCATTTCAGATTATTGTCAAGATATTAGAT  
GTTTGTACATTTAAAAATTGCTCTTAATTAAACTCTCAATACAATATATTGACC  
TTACCAATTCCAGAGATTCACTGAGCTTAAATTTAAACTCTCAATACAATATATTGACC  
AAACAATATAATATTTCTAAACACAATGAAATAGGGAATATAATGTATGAACCTTGCAT  
TGGCTGAAGCAATATAATATTTGTAACAAAACACAGCTCTTACCTAATAAACATTAT  
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA AAAAAA  
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

## **FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNNGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKIGKSCKCSKGYQGDLCSPKVC
EPGCAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
```

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## **FIGURE 5**

CGGACGCGTGGCGTCGGCGGTGCAGAGCCAGGAGGCCAGGAGGCCACCATGTGGCGATGTCCACTGGGCTAC  
CCCCAGCCCACACCTCACCAGGGCCCAGGAGGCCACCATGTGGCGATGTCCACTGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCTGGGCCGG  
GAGCTAGCACCGGGCTGCACCTGCAGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGCGTGCAGACTGTGCCCTGCCCTACCTGGCGCCATCT  
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTTGGAACGTACTGGGACAACGTAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGGCCCTCTGGGCATGACTGAGGGCATTGCTACCGCTGGCACCA  
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGCTGAACCCAGGGAG  
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAACCTGATTGATGAGCCTCTTGA  
CCAAGGCAACTGTGAGGCTCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCGTCTGCTGCCCCAGAACCTGCTGTCTTGAC  
ACCCACCAGCAGCAGGGCTGCCCGGTGGCGTCTCGATGGTGCCTGGTGGTCTGCC  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTGGGCCTGAAACGAGACGAGGCTGGC  
CTGCCCTGTATGATGACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAATAACATGACATCTACCAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCAGGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTATAACAGGGAGGCATCTACAGCCACAGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTAAATACTGACTGCCCAACTCCTGGGCC  
CAGCCTGGGCGAGAGGGCACTTCCGCATCGTGCCTGGCTCAATGAGTGCACATCGAG  
AGCTCGTGTGGCGTCTGGGCCGTGGGATCCAGGCTAAGGGCGGCCAGGGCCAATG  
GGCGGTGACCCAGCCTCGCCGACAGAGGCCGGCGCAGGCCGGCGCAGGGCGCTAAT  
CCCGCGCGGGTCTCGTACGCAGGCCCGCCTGGGAGGCCGGCAGGGAGACTGGCG  
GAGCCCCAGACCTCCAGTGGGACGGGGCAGGGCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCCTCTGGGCCCAACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCACCCAACTCCGTATTCTTTTTTTAGACAGGGTCTGCTCCG  
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGTTCA  
AGTACCCCTCCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCCACACCTGGC  
TAATTTTGATTTTGAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCAACT  
CCTGGCTCAAGCGGCCACCTGCCTCCGCTCCAAAGTGCAGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGATTCTATTCTCAGATATTATTTCTTCACTGTTAAAAA  
TAAAACCAAAAGTATTGATAAAAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYEQDLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCGTCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTATGGAGG  
TGCATGAGGACTTCTTCCCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTGGG  
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCTTGCCTGCAGCCAGGCAGTCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACC CGCGCATCCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCACTGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCCTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT  
CCCTGCCAACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAAACTGGA  
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTGCTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAAA

## **FIGURE 9**

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT  
DPPADGPSNPLCCCFHGPAGFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCACCGCGTCCGAAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTGAGGGACCAGGGGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGAACAGGAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG  
CGTGGTCACGGAGATCGTGCTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCCAGGGCGGCCAGGCTCCGCAGCCGCCAGAAC  
CAGCGCAGGCCCACTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC  
CGAGAACAGAACAGCAGTTCGAGTTGTGGCTCGCCCCACCCGCCGGACCAAGCGCACAC  
GGCGGCCCAAGCCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCCTGGCCGCCCTCCC  
CACCCCTTCCCTTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC  
GAGGGAGGACCCCTGAGGGCCGCAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG  
CCCCAGGGCGGCTGGCACAGTGCCCCCTCCCGACGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGCTCTGAAGCC  
CGCTGAAAGGTCAAGCAGTGAAGGCCTTGAGACAAACCGTCTGGAGGTGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCCAAACTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGGAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCCACCCCAACTCCCAGCCC  
CGGAATAAAACCATTTCCCTGC

## **FIGURE 11**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRKGKLIGKPSGKSKDCVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## **FIGURE 12**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTTTGCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCACAGAACCCCATCCAGT  
CATTGATTGCTGTTATTTTTCTTTTCTTCCCACACATTGTATTTAT  
TTCCGTACTTCAGAAATGGGCTACAGACCAAAAGTGGCCAGCCATGGGCTTTTCT  
GAAGTCTTGGCTTATCATTCCTGGGCTACTCACAGGTGTCAAACCTCTGGCCTGCC  
CTAGTGTGTGCCGCTCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG  
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAAATTAAATGC  
TGGATTTCCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTCCAAGAATGTCAGAGTTCTCCATTGCAAGGAAAAC  
AATATTCAAGACCATTTCACGGGCTGCTTGGCCAGCTTGAAGCTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCCTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCCTGTTGGCTTCCGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGCCCTCCAGAA  
TCTCACGAGCTGGAGCGTCTTATTGGACGGAACCTCTGACCAACAAGGGTATGCCG  
AGGGCACCTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAACGTAATTGCTGTCC  
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAAGAT  
AAACCACATTCCATTGACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTGATAATCTCTCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCCCTGGTTTGTGACTGCAGTATTAAATGGGTCAACAGAATGGCTCAA  
ATATATCCCTTCATCTCAACGTGCGGGTTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCCGTAGGGAATTAAATATGAATCTTGTCCCTGCCCACACGACCCCCGGCCTG  
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCGACCAACTCAGCCTCCACCCCTCTAT  
TCCAAACCCTAGCAGAAGCTACACGCCCTCAAACCTACCCACATCGAAACTTCCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGACCCCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTGTAATGATACTTCATTCAAGTCAGCTGGCTCTCTCTTCAACCGTATGGCATA  
CAAACTCACATGGGTGAAAATGGGCCACAGTTAGTAGGGGGCATGTTCAAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTACTTAGAGCCCCGATCCACCTATGGATT  
TGTTAGTGCCACTGGATGCTTTAACTACCGCGCGTAGAAGACACCAATTGTTCAAGGC  
CACCAACCATGCCCTTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT  
GTGCTGGTGGCTTGTCTAGCGTCTTGTGGCATATGCACAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGCCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTCAGATCGTCTCTTAAATAACGAT  
CAACTCCTAAAGGAGATTCAGACTGCAGCCATTACACCCAAATGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCACACCTGGAGC  
ACTGCCATACGTGACAGCCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGACATCAAAGACACGCAGATTACATTGATAAAATGTTACACAGATGCAT  
TTGTGCATTGAAATACTCTGTAATTATACGGGTACTATATAATGGGATTAAAAAAAGTG  
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACTCTTGCTTTAAATCTT

## **FIGURE 13**

MGLQTTKWP SHG AFFL KSWL IIS LGL YSQV SKLL ACPS VCR CDRN FVY CNERS LT SVPL GIP  
EGTV VL YLHN NQIN NAGF PAEL HNV QSV HTVY LYGN QLDEF PMNL PKN VRVL HLQ ENNI QT  
SRAA LAQLL KLEEL HLDD NSI STVG VEDG AFRE A ISLK LLFL SKNH LSS VPV GLPV DLQ ELR  
VDEN RIAVI SDMA FQNL TSLE R LIVDG NLL TNKG IAEGT FSHT KLKE FSIV RN SLS HPPP D  
LPG THLIR LYLQDN QINH I PLTA FSNL RKL ERLD I SNN QL RML TQGV FDNL S NLK QLT AR NN  
PWF CDCS I KWV TEWL KYI PSSL NVRG FMCG QGPE QVRG MAV REL NMN LLS CPTT PGLPL FTP  
APST ASPTT QPPT LSIP NPNS RSYT PPPT SKL PTI PDWD GRER VTPP I SERI QLSI HFV ND  
TSIQ VSWL SLEFT VMAY KLT WVKM GHSL VGGI VQER IVSGE KQHLS LVN LEPR STYR IC LVPL  
DAFN YRAVED TIC SEAT THAS YLN NGNS NTASSHE QTT SHSMG SPF LLAGL IGGAVI FVL VVL  
LSVFCW HMKK GRYT SQKWK YNRG RRK DDYCE AGT KK DNSI LEMT ET SFQIV S LNND QLL KG  
DFRL QPI YTPNGG INY TDCHI PNN MRYC NSS VP DLE HCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,

522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## **FIGURE 14**

ACTTGGAGCAAGCGCGGCGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCGTCCTGCCCTCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGCGAGGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCTGCC  
TCGCTTCCCAGGCAGGCCGGCTGCAGCCTGCCCTCTGCTCGCCTGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTTCTGCTGATCCTCGGACAGATCGCCTCCCTGCCGAGGGAGCGGTACGTGGGAGGTCCATCT  
CTAGGGGCAGACACGCTCGAACCCACCCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAGCAGGGCAGACC  
TGGTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATGTGGACA  
TCTTGCATTCTGGACATTGGCTCTGATGTCACCCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGGCATCTGTCACGG  
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGCAGAGGGGGCCGGCCCTGA  
GGGAGAATGTGCCACGGGTATAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA  
AGGCACGGGACACGGGCATCTTAATCTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
GGAGTGGAGCCCATGAGGACCATGTCCTCTGTGGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGCACGGCCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCTACTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAACATCCAGGATCTGT  
GTGCCATGGAGGACCAACTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCCTCGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGTGGGAAGAGGTGTGGACTACTGTGCCCTAGAAAACACGGATGTGAAC  
ATGAGTGTGAAATGCTGATGGCTCCTACCTTGCCAGTGAAGGATTGTCTTAACCCAGATGAAAAAA  
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACGGGCTGTGAGCATGAGTGTGTCACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACACCTGCAGCCAGTGGACACTGTGAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTAACACGGAGGATTCTCGTGTGAGTGAACATGGGTGTGAATACTCCT  
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGAACATGGGTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTGCTGTGAGGGACACGTGCTCCCGAGCGATGGGAAGACGTGTG  
CAAAATTGGACTCTTGCTCTGGGGACACGGGTGTGAACATTGCTGTGAAGCAGTGAAAGATTGTTGTG  
GCCAGTGCTTGAAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAAGAGAAAGATGTCGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACACGTGCGAGTGCTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTGCAATCAACCCACCATGGCTGCGAACACATTGTGTTA  
ATAATGGGAACTCCTACATCTGCAAATGCTCAGAGGATTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCAATTGACCTGGTCTTGATGATGGATCCAAGAGTCTTGAGAAGAGAATTGGAGGTG  
TGAAGCAGTTGTCACTGGAATTATAGATTCCCTGACAATTCCCGGAAAGCCGCTCGAGTGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAAGGGCTTATGACTGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAAG  
GAGAAGGGCCAGGCCCTTCCACAAGGGTGCAGAGCAGCCATTGTGTTCAACGGAGCGGGCTCAGGATG  
ACGTCCTCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTTGTTGAGGAAAGCCATTG  
AGGAGGAACACTACAAGAGATTGCTCTGAGCCCACAAACAAGCATCTTCTATGCCGAAGACTCAGCACAATGG  
ATGAGATAAGTGGCAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGGAACGTGCAAAACGGTCCAACAGCCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTGCAACAGATATCTGTTGAAGAAGACAATCTTACGGCTACACAAAAGCTTT  
CCCATTCAACAAACCTCAGGAAGCCCTTGGAGAAAACACGATCAATGCAATGTGAAAACCTTATAATGT  
TCCAGAACCTGCAAACGAAGAAGTAAGAAAATAACACAGCGTTAGAAGAAATGACACAGAGAATGGAAGGCC  
TGGAAAATGCCCTGAGATACAGATGAAGATTAGAATCGCGACACATTGTTAGTCATTGATCACGGATTACAAT  
GAACCGAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATAACACTAACCTGTATAAATTATCTAGGAAAAAAACCT  
TCAGAATTCTAACAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAATATACTGTGGACAC  
AACTGCTCTGCCATCCTGCCATTGCTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT  
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTAACCTGTGGAACAAGTGGATTAAATACAATATTAAAATTCACCACTTCAG

## **FIGURE 15**

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGHRARTHPTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRKQGYILNSDQTCRQDLCAMEDHNCEQLCVNPQGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC  
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDBGKTCAKLDSALGDHGCE  
HSCVSSEDSFVCQCPEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFR  
LAEDGKRCRCKDVCKSTHHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKKCTEGPIDLVFVID  
GSKSLGEENFEVVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEELQEIASEPTNKHLFYAEDFSTMDEISEKLKGICEALEDSDGRQDS  
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEIDLRLSTQKLHSTKPSGSPL  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAGCGGCTGGCTCCCGCGCACGCTCCGGCCGCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGGC  
CATGATTCCTCCCTCCGGGCCCTGGTGACCAACTTGCTGCGTTTTGTTCTGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGCCAGCTGCAACTGCAC TGCCC GCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGAGGTGTCTC  
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGT CCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT  
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG  
GGTCTTTAACGCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCAGGCCAC  
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAAGTGAGCACAGGGCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGGTACCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTTGTACCACCGCCGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCGAACCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCC  
TTCCTCTGTACCTCCGCACGAGCCCTCCGCCACCCATGGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAAGCTGGCTCTGGTATTGATGAC  
CCCACCACTCATTGGCTAAAGGATTGGGTCTCTCCTTCTATAAGGGTACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC  
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCACCCACCCACTGACTCCTCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTCAAGTCTCCAGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC  
TTATTAAAACATGAAATATGTGTTGTTTCAATTGCAAATTAAATAAGATAACATAA  
TGTGGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKPQAVYQ  
WDRQLPSFQTFFAPALDVIRGSSLTNLSSSMAGVYVCKAHNEVGTACNCNTLEVSTGPGAA  
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTLWPWPKSSDTISKNGTL  
SSVTSARALRPPHGPPRGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## **FIGURE 18**

CGCCACCACTGGGCCACGCCAATGAAACGCCTCCGCTCCTAGTGGTTTTCCACTTG  
TTGAATTGTCCTATACTCAAATTGACCAAGACACCTGTCTCCAAATGAAAATGTGA  
AATAACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCTGTGGCGAAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA  
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGTGCCATT  
TAGATAATGTCTGTATAGCTGAAATATTAAATAAAAACCTTAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATAGAAATTAGCTGAATCATCTCATTACTAGGTACAAGAACAAACA  
CTATCTCAGCCAAGGACACCCTTCTAACTCAACTCTTACTGAATTGTAACCGTGAAT  
AATTGGTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAATCATGCACACTGTTGAACAAGCTACTTAAAGGATATCCCAGAGCTTCC  
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTCTTTTGAT  
TCATATAACATGAAACATATTCTCATCTCATATGAATATGGATGGAGACTACATAAATATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGAATGTCAGTGCATTGATTTATATTATA  
AGAGTATTGGCCTTGTCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCTAGTCTCAATGAGCTCAAACCC  
ACCCACATTATATGAACATTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA  
GGTATAGGAGTCTATGTCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAGATTATAATATT  
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTCATTGCTTGCCATATGCATT  
ACCTTCTGGTCTTCAGTGAATTCAAAGCACCAGAACACAATTCAAACAAATTCTTGCTG  
TAGCCTATTCTTGCTGAACTTGTTCTTGTGGATCAATACAAACTAAAGCTCT  
TCTGTTCAATCATTGCCGGACTGCTACACTACTCTTTAGCTGCTTGCATGGATGTGC  
ATTGAAGGCATACATCTATCTCATTGTTGTGGGTGTCATCTACAACAAGGGATTGGCA  
CAAGAATTTTATATCTTGGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC  
TAGGATACAGATATTATGGCACAAACAAAGTATGTTGGCTTAGCACCAGAACACTTTATT  
TGGAGTTTATAGGACCAGCATGCCATTCTGTTAATCTCTTGGCTTTGGAGTCAT  
CATATAACAAAGTTTCTGCACACTGCAGGGTTGAAACCAAGTTAGTTGCTTGAGAAC  
TAAGGTCTTGCAAGAGGAGGCCCTCGCTCTGTTCTCTGGCACACCTGGATCTT  
GGGTTCTCATGTTGTGCACGCATCAGTGGTACAGCTTACACTCTCACAGTCAGCAATGC  
TTTCCAGGGATGTCATTGTTATTCTGTGTGTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTCAAAATGCCCCGTGTTGGATGTTAAAGGTAAACATAGAGAATG  
GTGGATAATTACAACACTGCACAAAATAAAAATTCAAAGCTGTGGATGACCAATGTATAAAA  
TGACTCATCAAATTATCAAATTATTAACACTAGACAAAAGTATTTAAATCAGTTTCT  
GTTTATGCTATAGGAACACTGTAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT  
TTTCTATGTGAAATAGTCTGTCAAAATAGTATTGCAAGATATTGGAAAGTAATTGGTT  
CTCAGGAGTGTATCACTGCACCCAAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA  
TGTCTGAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC  
CCTACCACCTCGGTAAATGAGCTCATTACAGAAAGTGGAACATAAGAGAACAGGGCAGA  
ATATCAAACAGTGAAGGAAATGATAAGATGTATTTGAATGAACACTGTTTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAAACACATTACCAATTGAA  
TTGTTCTGAACCTAAATGTCCACTAAACAACTTAGACTCTGTTGCTAAATCTGTTCTT  
TTCTAAATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 19**

MKRLPLVVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGSGNGVTICEDDNEC  
GNLTQSCGENANCTNTESYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNV CIAA  
NINKTLTKIRSIKEPVALLQEYVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTERFVKT VNNFVQRDTFVWWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT  
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAA YDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF  
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTTRITQLG  
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAEVFLVGINTNTNKLFCIIAGL  
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT  
TKVCWLSTENNFIFS FIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKI QEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTCAGTTTATTTAAGAGTAT  
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCAC  
ATTATATGAACTTGAAAAAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTACAA  
GGATCACTCAACTAGGAATAATTATTCAGTGATTGTCTGCCATATGCATTTTACCTTC  
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

## **FIGURE 21**

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCCTCCCGCAGATCCGAACGGCCTGGCGGGGTCAACCCGGCTGGGA  
CAAGAAGCCGCCGCCTGCCTGCCCGGGCCGGAGGGGCTGGGCTGGGCCGGAGGCAGG  
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTGGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG  
CCGCCGCCGCGTCAGAGCAGGAGCGCTCGCTCAGGATCTAGGGCACGACCATCCCAACCC  
GGCACTCACAGCCCCCGCAGCGCATCCCGTCGCCGCCAGCCTCCCGCACCCCCATGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCGTGGCCGGCGCCCCCTGCCTCTCGACGCGGGCC  
CCACGTGCACTACGGCTGGGCGACCCCATCCGCCTGCACCTGTACACCTCCGGCCCC  
ACGGGCTCTCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTGGACTGCGCGGGGC  
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTTGCGGACCGTGGCATCAAGGG  
CGTGACAGCGTGCCTGACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCCTCCGGCTCCCTGAGCAGTGCCTACAGCGGAGCTGTACAAGAA  
CAGAGGCTTCTTCCACTCTCTCATTCTGCCTGCCATGCTGCCATGGTCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAACT  
GAGACCATGCCCGGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG  
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA  
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCTAGCTAGCAATAGACTGTCTGAT  
CATACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGCCCCATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTGAATACTCCATCGATGGGAAC  
TCACCTCCTTGAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTCAGGAACAGGTGATCCACTCTGTA  
CCCAGGAGCAGCCAGAACAGACAGGCAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG  
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCAAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC  
CTGAGGCCAGTCTGTCAATGGATGCTGCTGAGAATAACTTGCTGTCCCGGTGTACCTGC  
TTCCATCTCCAGCCACCAGCCCTCTGCCACCTCACATGCCTCCCATGGATTGGGCCT  
CCCAGGCCCCCACCCTTATGTCAACCTGCACCTTGTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCAAGTCTTGTCAATAACTTGCTGTGGAAGCAGCGGGGAAGACCTAGAAC  
CCTTCCCCAGCACTGGTTCCAACATGATAATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTCTTACATTATTATGCCCAAATTATATTATGTATGTAAGTGGAGGTTG  
TTTGTATATTAAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVRSEKHRLPVSLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCAGAAGTTCAAGGGCCCCGGCCTCTGCGCTCCTGCCGCCGGACCCCTGACCTCCTCA  
GAGCAGCCGGCTGCCGCCGGAAAGATGGCAGGGAGGAGCCACCACGCCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTAGCCTGAAAACCCAA  
AGAAGACTGTTCCCTCAGATTAGAGTGAAGAAACTGGGTGGAGTGTCTCCTTGCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATAACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAGA  
CAAAGAAGGAAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAACGGAACT  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCGCAATT  
TGTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCCTCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGAATGTGCAGTGGCTACGCCTGTAATCCAGCAGTTGGAAAGG  
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGGCAGTCTGCCAATATGGTAAACCC  
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAATAAATAAATA  
AATAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

## **FIGURE 24**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDOQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRLGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNI SGIIIAVVVVA  
LVI SVCGLGV CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA AAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## **FIGURE 25**

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACAGCCGGACCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAACATGGATTAAATATTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTACATACTCCACCTTCAAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTAACCTCTCTCCAATATGCATGACATTTGGACAATG  
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA  
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACCTACTAGCACTGACTG  
TGGATCCTTAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCATGTGCTACTTGGCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAATCAGGCCTGGTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTAACTTCCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCTCACAGACTAACAAATATTGCAAAATTGAATACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT  
ATTAATGTAAAAAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTTACTGA  
ACTGCCTGAAAAAATGTCGTCCGAACGTGAGCAACTTACAAGAACTCTATATTAAATCACAACT  
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCTACATAATCTTCTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT  
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTTTATCA  
ATCTTCGCAGCCTGGTATAGCTGGTATAAACCTCACAGAAATACCAAGATAACGCCTTGGTT  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGGCTTATTAAAGTACCCCATGT  
TGCTCTCAAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA  
TACGAAGGGGTGATTTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATAATATGCCT  
GAGCTGATTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAATAGAAGC  
TACTAACAAACCTAGATTGTCTTACATTCCCCAATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCTGGTACCTG  
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG  
GATGAACATGAACAAAACCAACATTGATTCTGAGGCAACTGTTGGACATTGTTGCGTGGACC  
CACCTGAATTCCAAGGTCAAGAATGTTGGCAAGTGCATTTCAGGGACATGATGAAATTG  
CTCCCTCTTATAGCTCCTGAGAGCTTCTTAATCTAAATGTTAGAAGCTGGGAGCTATGT  
TTCCTTCACTGTAGAGCTACTGCAAGAACACAGCCTGAAATCTACTGGATAACACCTCTG  
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA  
GATATAAAATGGCGTAACTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG  
GCTCTTGAATATTAAGAGATATTCAAGGCCATTCACTGGATTTGGTGTCTGGAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA  
TGCTGCGAAAGTGTGCAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTATCAGAAAACAGAAAAAAA  
TGTGTAAATGTCACCACCAAGGTTGCAACCTGATCAAAGAGTATGAAAAGAATAATAC  
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTATAATCTGGGAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCCT  
AAAAACCACCAAGGAAACCTACTCCAAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNIAKIEYSTDGPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSVLVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVNLKFIDLNKNPINRIRRQDFSNMLHLKELGINNMPELISIDS LAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSA LYHGTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRFQHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC  
IATNLVGADLKSVMIKV DGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV  
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVN VTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNC DGGHSYVRNYLQKPTFALGELYPP LIN  
LWEAGKEKSTSLKV KATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGC**ATGA**ATCT  
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCAACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTCAATAACCTGAAGGCCAGGGCAGAATTGCCAACACCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGAAAACGTCCGTGTTGGATGAAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTGTTGGCTGGTTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAACGAGGAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGT**A**TAGTGTCCAACACTGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTGCGATTGCACTAGAAATAAGTGGTTACTTCTCCCATCCATTGTAAACATTGAA  
ACTTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTT  
AATTAAAAGCAAATAAAAGCTTAACTTGAACCATGGAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLSSSGGLNVTC SANLKEIPRDL  
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNICKTSVLDEHAGR PFL  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

ACCGAGCCGAGCGGACCGAAGGCAGCAGATGCAGGTGAGCAAGAGGATGCTGGGGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCTGGCAGCCCATTCTCTGCTGGTGTCT  
GGGCTCAGTGTCTCAGGCTCGGCCACGGCTGCCGCCCCGCTGCGAGTGTCTCGCCCAGG  
ACCGCGCTGTCTGCCACCGCAAGTGTCTTGAGTCAGTCCCCGAGGGCATCCCCACCGAG  
ACGCGCCTGCTGGACCTAGGAAGAACCGCATCAAAACGCTCAACCAGGACGGAGTTGCCAG  
CTTCCCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTAGCGCCGTGGAGGCCCGCG  
CCTTCACAAACCTCTCACCTCCGGACGCTGGGTCTCCGCAGCAACGCCCTGAAGCTCATC  
CCGCTAGGCCTTCACTGGCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT  
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTGGAGGTGGCG  
ACAATGACCTCGTCTACATCTCACCGCGCCTCAGCGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT  
CATCGCTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC  
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAC  
TGCCTCTACGCCCTCACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCCGCCACCTAGTCTATCTCGCTTCCTCACCTCTCCTACAACCCATCA  
GCACCAATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGGGC  
GGGCAGCTGGCGTGGTGGAGCCCTATGCCCTCCGGCCCTCAACTACCTGCGCGTGTCAA  
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCACTCGTGGCAACCTGG  
AGACACTCATCTGGACTCCAACCCGCTGGCTGCGACTGTCGGCTCCTGTGGGTGTCCGG  
CGCCGCTGGCGCTCAACTCAACCGGAGCAGGCCACGTGCGCCACGCCAGTTGTCCA  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGCCACACGGTGCAGTT  
GTGTGCCGGGGCATGGCACCAGCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGGGCAACGCCGGCAACGAC  
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGGCCCCATAGCCAAACAA  
GACCTCGCTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCGCGCCACTG  
TGCCTTCCCTCGACATCAAGACCTCATCATGCCACCACATGGGCTCATCTCTTTC  
CTGGCGTGTCTCTGCCCTGGTGTCTGTTCTGGAGGCCGGCAAGGGCAACAC  
AAAGCACAAACATCGAGATCGAGTATGTGCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG  
ACGCCGCCCAAGTTCAACATGAAGATGATATGAGGCCGGGGCAGGGACCCCG  
GGCGCCGGGAGGGGAAGGGCCCTGGTCGCCACCTGCTCACTCTCAGTCCTCCACCTC  
CTCCCTACCCCTCTACACACGTTCTTCTCCCTCCGCCCTCCGTCCCCTGCTGCCCG  
CCAGCCCTACCCACCTGCCCTCTTCTACCGACCTCAGAACGCCAGACCTGGGGACCCCA  
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC  
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTGGGTTCAATAATTATGGATTT  
TATGAAAATTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELENENIVSAVEPGAFNNLFNLRTL  
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLMINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTLEESVFHSVGNLLETLILDSENPLA  
CDCRLLWVFRRWRNLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL  
CIAANAGGNDSMPAHLHVRSYS PDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## **FIGURE 31**

CCACCGCGTCCGACCTCGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCAGCCGCCTCGCTCCTGCTCCTGC  
TGTTCGCCTGCTGCTGGCGCCGGCGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGCTCAAGTGCCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCGT  
GCGAAGTCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTACCAAGAACTCCACGGAGAACCAACCGCAT  
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCAGTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCCGAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGGAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTCCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGTGGATCGTGGCTTCATTGTCTCCTGCTG  
CTCATCATGCTCATCTCCTTGGCCACTACTTGATCCGGACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGGACACGGCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCATAGAGGCGCCTGCCACTTCTGC  
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAATGTCTG  
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTG  
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGTGAGAAAAGCAAAAACA  
AACAAAAAACA

## **FIGURE 32**

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 33**

GGGGGTTAGGGAGGAAGGAATCCACCCCCCACCCTTCAACCCCTTTCTCCTTCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGTAATTGTGTCGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATGGGGATGAATTGCTCGCTTAAAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCCTTGTGCGCTGAAACGTTACAGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCATTTATTCTGCATGGCAATT  
CCTCACTCGACTTTCCAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG  
AAAACAATGGCTTGATGAAATCGTCCGGGGCTTCTGGGCTGCAGCTGGTAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTCCAGG  
ACTTGAACACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGAAAACATTCCAAGAATGCC  
CTGATCGGCCGAGTGGCTGCAAGGCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGTCCTTGAAAACCGAGTGGATTCTAGTCTCCGGCGCCCC  
CCCAAGAAGAGACCTTGCTCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGGCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC  
GTTTACCCCTGCCCTGGGGCTGCACTGCGACCACATCCCAGGGTGGTTAAAGATGAAC  
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA  
GCTTTCTACAGAGATAACAAGATCCACAGCATCGAAAATCGACTTGTGATTACAAGA  
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGTACTGTAGAGAACAAACTTCAAG  
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCC  
GAAATTGCGGGGCTGAAAACCTAGAGTACCTGAACGTGGAGTACACGCTATCCAGCTA  
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACAAACCTG  
CTGAGGTCCCTGCCTGTCGTGGACGTGTTCGCTGGGTCTCGCTCTCTAAACTCAGCCTGACAA  
CAATTACTCATGACCTCCGGTGGCAGGGGTGGACCTGAGTTAACCTCCATCATCCAGA  
TAGACCTCCACGGAAAACCCCTGGAGTGCTCTGACAATTGTCCTTCAAGCAGTGGCA  
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAAC  
TAGAAAGGATTTCATGCTCCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCACGTTACTCGCACAGTAAAACAGCACTGGTTGGCGAGACGGGACGCACTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCGGGACTGCTGCTGGT  
GTTTGTACACCTCCGCCTCACCGTGGTGGCATGCTCGTGTGTTATCCTGAGGAACCGAAAGC  
GGTCCAGAGAGAGATGCCAACTCCTCCGGTCCGAGATTAATTCCCTACAGACAGTCTGT  
GACTCTCCTACTGGACAATGGCCTTACAACGAGATGGGCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAAAGACCCCAACCCAAATAGGGGAGGGCAGAGGGAAAGGCG  
ATACATCCTTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCAAATCCCC  
CCATCAGCCTGGATGGCATAAGTAGATAAAATAACTGTGAGCTCGCACACCGAAAGGGCT  
GACCCCTTAATTAGCTCCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA  
GCCAGCTCGCTTTGCTGAGAGCCCTTTGACAGAAAGCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCCTGCCCTCGGCCCCGGGGCTGTGGGTTGGATGCCCGGGTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTCTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAATAAGTAACCTTGACTTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGVCCKEKCSCNEIEGDLHVDCCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPYEEVLEQIPGIAEILLEDPNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDNLNETTEQDLCPLKNRVDSSLAPPAPPAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGT  
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSCDHIPGSGLKMNCNNRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYNIAIQILIPGTFNAMPKLRILILNNNLLRSILPVDVFAGVSL  
SKLSLHNNYFMYLPPVAGVLDQLTSIIQIDLHGNPWECSCTIVPKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL  
VPGLLLTVFVTSAAFTVVGMLVFIIRNRKRSKRRDANSASEINSLQTVCDSYWHNGPYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## **FIGURE 35**

AGTCGACTGCGTCCCCGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGACACATTCTGTGCGGGCTAACGGAAACTGTTGGC  
CGCTGGGCCGCGGGGATTCTTGGCAGTTGGGGTCCGTCGGGAGCGAGGGCGGAGGG  
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTACCGCCTCAGACAC  
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG  
AGAATGAGGCCGGCGTTCGCCCTGTGCCTCCTCTGGCAGGGCCTCTGGCCCGGGCGG  
CGCGAACACCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGCGCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGGCAGGGAGGAGCCTGCATCCTGCGAGGTGGGCGCTC  
AGCACCGTGCCTGGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCTGCGGGAGGCCAGG  
GCCGGAGGGGCTCAAAGACCTGCTGTTCTGGGTCGCACTGGAGCGCAGGCGTTCCACT  
GCACCTGGAGAACGAGCCTTGCGGGTTCTCTGGCTGCTCTCGACCCCGCGGTCTC  
GAAAGCGACACGCTGCAGTGGTGGAGGAGCCCCAACGCTCCTGCAACCGCGGGAGATGCGC  
GGTACTCCAGGCCACCGTGCGGTCGAGCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGTACCTGTCAAGTACCAAGTGGTCTTGAGGTCTTGCTGCTCGCCGCCCGG  
GCCGCTCTAACCTTGAGCTATCGCGCCCTCCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTGCA  
TCGCGACGAAATCGGCCGCTCGCTGGACAAACTCTGGCGATGTGTTGTCCTGCC  
GGGAGGTACCTCGTCTGGCAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTGGGAGG  
CTTGCCCTGCAATGTGCTACGGCTTCGAGCTGGGAAGGAGCGCCGCTTGTGACCA  
GTGGGAAGGACAGCGACCCCTGGGGGACCGGGTGCCCCACCAGCGCCCGGCCACT  
GCAACCAGCCCGTCCGCAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC  
ACCACTGTCCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTCCAAGTTAAATTCTACGACTCCTCTGCCACTCCTCAGGCTT  
CGACTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTGTGTTGGTGTCT  
TGACCATGACAGTACTGGGCTTGTCAAGCTGTCTCACGAAAGCCCTTCCCAGCCA  
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGTGAGCCCCTGCTTGGCT  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAGTCGGGACTGTGATCTGCCAGAG  
CAGAGGGTGCCTTGTGGCGAGTCCCTTGGCTCTAGTGATGCATAGGGAAACAGGGAA  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC  
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA  
TGGTGATACTGGGGACGGTAGTGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA  
TTGGAGAAGTGTGAACTTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA  
TTAAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT  
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAATTTAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWP GP GGG EHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYCKYQFEVLCAPRPG  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGFFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDPEPAALGSSSAHTNNGVKGDCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## **FIGURE 37**

CGGACGGTGGATTCAAGCAGTGGCTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATGCCTTAAAGTGCCTCCGCCCTGCCGGCGGTATC  
CCCCGGCTACCTGGGCCCGCGCGGTGCGCGCGTGAAGAGGGAGCGCGGGCAGCCGA  
GCGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGTGCAGA  
GGGGCGTGTGCGCGCGCGCGTGGGTGCAAACCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGTGCAGCCACCCAGCTCTCGCG  
CAGCAGTCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA  
CAGTCCCAGAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCATGCCAATGCCAGCGATTGCCG  
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC  
CCCCAACTGGCCAGACGGGATTACCCCTGCAGGAGTCACCTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCACT  
TTTATCAGACTTAAGTTAAGTGCAGATGGTTATTGGTCACTACATATTCAAGGCCAAA  
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGTTAAA  
ACCCACCGTGGCCTTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGCAGCGGG  
CAAGAACATGAGTCCAGGCTGACTGTCGCTGCAAGCAGTGCCTCTCAGAAGAGGTC  
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATAGAACGCTCCTGGATGCCCTAAAAAATAAGCAATG  
TTAAACAGTGAACGTGTCATTAGCTGTATTCTGCCATTGCCATTGAAAGATCTATGTT  
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCTT  
TGCCTGCTGTCAAGAGGAGCAGCTATCTGATTGGAAACCTGCGACTTAGTGCAGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTATTACATCTCTGAAAGGAT  
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTAGAAGTGCATATTATAGT  
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGTCTGCGTTCTA  
AATCAATGCTTAATAAAATATTAAAGGAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVLNFRFIDLESNDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRTDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLDAKKNQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGGCGGTGCCTTCTT  
CCTCTCGTGGCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACTG  
CCGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACTTGGAG  
GTGGAAACACTGCCTGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGAACAGAGAGGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCGGCTACGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCCGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA  
ACTGTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA  
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTGGCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCACTGGTGTTCACCGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTCAAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGA  
ATCGCAGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCGAGAGCTTGGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTGGTTATTGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
CCTTACAGAGCAGGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTTCACTGGCGGGACTGGCAGGCTCACAATGTGTGA  
ATTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT  
TCTGTGTTCAACCACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA  
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPPPKGVLPAVLWGLSLFLNLP GPIWLQPSPPPQQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCPGTERPCGGYGCCEGTRGGSGHCDCQAG  
YGEACGQCGLGYFEAERNASHLVCASF GPCARCSGP ESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYE CRDCAKA CLGCMGAGPGRKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCEN TEGGYRCICAEGYKQM EGICVKEQI PESAGFFSEMTEDELVVLQQMFFG  
IIICALATLA AKGDLVFTAIFIGAVAAMTGYWL SERSDRVLEGFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCCTTGCTCCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTAAAGAGGT  
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG  
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGTCTTCAGG  
AGCCGGTCCCCAAGGCCGGCTGCACAGGCACGGGCGGCTGTCCCCGCGAGGCCCGGGCC  
CGGGTACCGTCGAGTGGCTGCCGTCCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCCGCTGGCGTCCGGCCACAAGCTGGTCCGCTTGCCTCGCAGGGGC  
GCCAGCCGGCTGGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG  
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTAAGTGGC  
CGTTTCTGGGCCTCGACAGTGCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCACAGGAGCTCCAGGCATAGGCGCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGAGGGTACCGAGGAGAGCTG  
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA  
GAGCCCTTGCAGTTCTATTCTATTACTGCACTATATTCTAACGACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCTGTCAC  
TGGATCTGGCTAAAGTCCACCACCTGGACCTAACGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTQPQVVS LPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTCGGGCTGTTGTCAAGTGGCCTGATCGCGATGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT  
GTGAAGTTGTCCGTGCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAGTTGACCA  
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGATGGTCTCTGAGGAAGGCGGAAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCCTGCCACCATGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAAAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT  
GGGATAGTGATGCCTACGAACAAAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT  
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCTGTCAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGTATGGACACCCATGACTTCAAATGCTGTGCGCATGGAAAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGCTTGTAAACCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGGCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGACCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT  
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTATTTGTCTTC  
TACACCCCACAGGGCCCCCTACTTCTGGATGTGTTTAATAATGTCAGCTATGTGCC  
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACCTGTTAAA  
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCTTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG  
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG  
CCACTGGATCCCTGCCCTGCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAAACCGCTGCTAAAGAAAAGAAAATGGAGGCTGGCGAGTGGCTACGCC  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAIIICSLALGSVTVHSSEPEVRIENNPKLSCAYSGFSSPRVEW  
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIQMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCGCGCTGTGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCGCTTCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG  
GCTCGTCCCACCAAGTCCAGTGCCGCACCAGTGGCTATCGTGCCCCCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTCAGGATTGAGCC  
ATGTACCCAGAAAGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAACTGCGCAACTGCAGCCCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGACCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGAAG  
GGGATGCCACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC  
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCTCTGCCGGAAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCAACGCCTATGGGTTATTGCAGCTGCTGCCGTGC  
TCAGTGCAAGCCTGGTCACGCCACCCCTCCCTTTGTCCCTGGCTCCGAGCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAC  
CTCGCTGCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGTGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCDRDLDSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL  
RNCSRRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCCACGCGTCCGGTCTCGCTCGCTCGCAGCGGCCAGCAGAGGTGCGCACAGATGCGG  
GTTAGACTGGGGGGGGAGGAGGCAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTG  
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT  
CGATGACCTTCAAGTGTGCTGACCCGGCATTCCGAGAAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTCTTGAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGAAACCTAGGCTGGATCCAAGTGA  
TAATTCCATCTGTGCAAGAACGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCA  
ACAAGACATATAGACATGGAGAGAACGCTAACATCACTTGTCACTGAAGGATTCAAGATCCGG  
TACCCGACCTACACAATATGGTTTATTATGTCGCGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTAGTCACGGAGATTCGTCT  
GCCACCCGGCCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTACTGCGATCCT  
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCCGGAG  
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTGGCTCATGCTCCGTCTATG  
ACGAAGCTGTGAGTGGGGCTTGAGTGCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTTTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTCGGACAACCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGGCCAGGCATCCATCATGCCACTGGGT  
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCCAAAGTGTCTGAAGTGTCTTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTCTTCTTGTTTAGACAAATGTAAACAA  
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPLICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFATSVLLVLLVILARMQTKFAHFPPRGPPRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCCACCGCGTCCGCTCCCGGCCCTCCCCCCCCTCCCGCTGCCGTCCGGTCCGTCGGTGGCCTAGAGA  
TGCTGCTGCCGCCGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCCGCTCCACGCCGT  
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG  
CCGTGCTGCTGCCGTGCTGGTGGGCTGCCGCCAGGGTCGCCTGCTGAGTGCC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCAGCTGCCGGGAGGGACACAGAGGCCTGTTA  
TAAAGTCATTACTTCATGATACTTCTCGAAGACTGAACCTTGAGGAAGCCAAGAACGCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCAGATGAACAGAAACTGATAGAA  
AAGTCATTGAAAACCTTGCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT  
CACAATTTAGGAACGGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACAAATTCATTGCAAATATTCTGATGAGAACACCAGCAGTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG  
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCTTGAATCTGGCTACAT  
CCTAATCCCCAGCATTCCCTCTCCTCCTGGTCACCACAGTTGTATGTTGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCCATC  
TGGCCCTCTCCTCACCAAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTCATTCCGAGTGTGTT  
CGGGAGAACCCACTCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA  
GTTCTCCCCAGACCAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG  
GTTATTAGGACATATAAAAATGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAGCCTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCTGGACCCCCACGTTGGCTGTATCCTTTAT  
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACTTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAAAGATGGCTGTGGAGCTTGGAAAACCACCTCTGTTCTGCTATACAG  
CAGCACATATTATCATAACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGCAATTCTCATATCTGTTTTCAAAGAACATAAAATCAAATAAAGA  
GCAGGAAAAAA

## **FIGURE 50**

MRPGTALQAVILLAVLLVGLRAATGRLLSASDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY  
SDEKPAVPSREAEGEETELTPVLPEETQEEAKKTFKESREAALNAYILIPSIPLLLLLV  
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTVTLVSVESGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCGCTGAGCCCCGGCGCCGCAGAAGACTTGT  
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACGGGGCTGGAGTCCCTCTCAAGCC  
GCTCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT  
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC  
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTAGAAGTCTTGTATCCAACCTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTATGATG  
TGACCTTCATACCGCTTAATGACCTGGGATTTGACCAAAATGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCAAGGGAAAGGAGCAGGTGCCAGAGGGTTGCCCTGATGGCTCTGCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAAGTGCCTTATAACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLQLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTASLQPGISEDLKKVKDRMGIDSSDKVD  
FFILLDNVAEQAHNLSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## **FIGURE 53**

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCAGCTGGTGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACTTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA  
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG  
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA  
GGATTGCCCTCTGGCCTTGGGAGAACACACCTGCAACCAGATGAAGACACGTGGTCG  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG  
GAGGTGCTGACAAGGGCTATGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA  
CCAGGGTGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCCCTCCTCAGAGACCGGA  
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGGAG  
CAGTCCCTGGAGCAGTGCAGCACAGATTGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
AAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTATACTTGGTCCCCCTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA  
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATAACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCAATTGCTCTGTTCTGAAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGTAATTGGTTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGTAACCTTATTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGLASPSGVRLVGGLHRCEGRVEEQKGQWGTVCDDGWDIKDVAVLC  
RELGCAGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQLMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDLW  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACCGCGTCCCGCGACCGGTGGCGGACCGTGCGGCCGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG  
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGTGCGCGGAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT  
GCGGGTGCCTAAACTGGTGCTCTGTGGCCGAATGGTGGGGCCCTAGAACAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGCCATAGTGCAGCAGCAGCTGAGATCCTGCAGTGCCTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA  
CTGTCTGCGTCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCAACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA  
CTCTGGCTCCTGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAACAGCAGCACTCTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTTGAGACTTTAATGGAGATTGTCTACAAGTG  
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAGGGCGGCCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKEAKVFYAAAGA  
KLVLCGRNNGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI  
VAAAEEILQCFGYVDIL  
VNNAGISYRGTIMDTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVN  
AITADGSRYGVMDTTT  
AQGRSPVEVAQDVLA AVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17



## **FIGURE 58**

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## **FIGURE 59**

CCCAACGGTCCGGGACGGTGGGTGACTAGTTCTAGATCGCAGCGGCCGCCGGCTC  
AGGGAGGAGCACCGACTGCGCCGACCCCTGAGAGATGGTGGTGCCATGTGAAGGTGATTG  
TTTCGCTGGTCTGTTGATGCCTGGCCCCGTGATGGGCTGTTCGCTCCCTATA  
CAGAAGT  
GTTCCATGCCAACCTAAGGGAGACTCAGGACAGCCATTATTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCCGGCCCTTCCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC  
TTCCCAGCTCAGATAACGCCAGAAGATGCCAGTAGTTCTCTGGTACAGGGTGGGCCGG  
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCTTATGTTGTACAAGTAACATGA  
CCTTGCCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTACTGATGATAACCACGGATATGCAGTCATGAGGACGATGT  
AGCACGGGATTATACAGTGCACTAATTCAAGTTCCAGATATTCTGAATATAAAAATA  
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA  
TGGATATTCTGATCCGAATCAATTATAGGGGGTATGCGAGAATTCTGTACCAAATTGGCT  
TGTTGGATGAGAAGCAAAAAGTACTTCCAGAACGCAGTGCCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCGACTAAC  
AAAGTACCTCTTACCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTGC  
GCACCGAACCTGAGGATCAGCTTACTATGTGAAATTGTCACTCCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACATAGTTGAAAAGTACTTGC  
AGATAACAGTACAGTCAAGCCATGGTTAAGTGAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAACGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAACGGCAGAAAAAAAGTTGAAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCAGGGTGA  
CTTCCATCAGGTAAATTATC  
GAGGTGGAGGACATATTACCCATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA  
TTCATTATGGAAAAGGATGGGATCCTTATGTTGGAAAACTACCTCCAAAAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTCATCAATAAAATTATCCTTGAAACAAAGTGAGC  
TTTGTTTTGGGGGAGATGTTACTACAAATTACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA  
AATTAGGGCTTGAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGGTGAGCTTG  
TAACAAACAAAGCTGTAAACATCTTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA  
TAGTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA  
AAAATATTATATAAAAAGTAAAAAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL  
VGPFPGNLNMKSYAGFLTVDKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLGDLTSDPSYFQNVTG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRO  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## **FIGURE 61**

CGAGGGCTTTCGGCTCCGGATGGCACATGTGGGAATCCCAGTCTGTTGGCTACAACAT  
TTTCCCTTCTAACAGTCTAACAGCTGTTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG  
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGAGGGCCTGCTAACAGCTTCAAAAAACAGGAGCGACTTCCACTGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAAGACTGGGTTAGTCCTAACATATCAAATTGACTGGCTGGG  
TGAACCTCAACAGCCTTTAACCTCTGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTGTAAAATAAATTAAAAAGCAAGTATTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTAACATTCTAACAGAGGGAGAAAGTATGTTAAAATA  
GAAAAACCAAAATGCAGAAGGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGTC  
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCCTGTGTTT  
GCAGAACATCATGTGAGGCCAACGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG  
ACAGCCGCTCTGGTCTGCTCAGTGGCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC  
ATGCCTCAGTCAGCACCTCCACTCTGAGAACATCGTACTGGACCTAACCAACTTGACCGT  
CCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCCTCATCGTCAGCCCTGCAGCGAAGTGTCAACCCCTACCAACAATGTCAACAAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTTACCAAGGGGCTGCA  
AGCTGCTGCGGCTGGATGACCTTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTTTCATCGGCACGGCTGTGGATGGAAGCAGGATTACTTCCGACCCCTGTCCA  
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGCCCTGGTCTCCACTTTGACAT  
CTTCTACATCTACGGCTTGCTAGGGGGCTTGTCTACTTCTACTGTCCAGCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGCG  
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGCTCCCTGCCCTGGCTGCACCCGGC  
CGGGGTGGAATACCGCCTCGCAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCCC  
AGGCCTTCAATATCACAGCAGGACGATGACTCTTGCATCTTCCAAAGGGCAGAAG  
CACTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGCCATCAACTT  
GCAGATCAAGGAGCGCTGCAGTCCTGCTACCAGGGCAGGGCACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGTCAGTGCACGAAGGCCTGCCCCATCGATGATAACTCTGTGGA  
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG  
TGGGACTAAGAGTGGCAAGCTGAAAAAGTAAGAGTCTATGAGTCAGATGCTCAATGCC  
ATTCACCTCCTCAGCAAAGAGTCCCTCTGGAAAGGTAGCTATTGGTGGAGATTAACTATAG  
GCAACTTATTCTGGGAACAAAGGTGAAATGGGAGGTAAAGAAGGGGTTAATTGTG  
ACTTAGCTTCTAGCTACTCCCTCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTCCAAACTTAAGAAAAACTTAAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTQHGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLAGSL  
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMYGVIIRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN  
LELNWLLGKD VQCTKAPVPIDDNFCGLDINQPLGGSTPV EGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESSLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## **FIGURE 63**

AGGCTCCGGCGGGCTGAGTGC GGACTGGAGTGGGAACCCGGTCCCCGGCTAGAGAACACGGC**A**TGACCA  
CGTGGAGCCTCCGGCGGAGGCCGGCCACGCTGGACTCCTGCTGGTCGTCTGGGCTCTGGTGCCTCC  
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGCGGCTCGCCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTCTGGATCTTCGGGGCTCCATCAACTATTTCCGTGTGCCAGGGAGTACT  
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGTGGCTTGAAACACCCCTACCACCTATGTTCCGTGGAACCTGCATG  
AGCCAGAAAGAGGCAAATTGACTTCTGGAACCTGGACTGGAGGCCTCGTCTGATGCCAGAGATCG  
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGAGTGGAGATGGACCTCGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTCACCGAAGCAGTGGACCTTATTTGACCACC  
TGATGTCCAGGGTGGTGCACCTCCAGTACAAGCTGGGGACCTATCATTGCCGTGCAGGTGAGAATGAATATG  
GTTCCATAATAAAGACCCCGATACATGCCCTACGTCAAGAAGGCAGTGGAGGACCGTGGCATTGGAACACTGC  
TCCTGACTTCAGACAACAAGGATGGGTGAGCAAGGGATTGTCCAGGGAGTCTGGCCACCATCAACTTGAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTTAACGTCAGGGGACTCAGGCCAAGATGGTATGGAGT  
ACTGGACGGGGTGGTTGACTCGTGGGGAGGCCCTACAATATCTTGGATTCTCTGAGGTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGGCTCTCCATCAACCTCTACATGTTCCACGGAGGACCAACTTGGCTTCATGAATG  
GAGCCATGCACTTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG  
ATTACACGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGCATCCCTCCCTCCCCACCTG  
ACCTTCTCCCAAGATGCCATGAGCCCTTAACGCCAGTCTGTACCTGTCTGTGGAGGCCCTCAAGTACC  
TGGGGAGCCAATCAAGTCGAAAAGGCCATCAACATGGAGAACCTGCAGTCATGGACAGTCCT  
TCGGGTACATTCTCATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCTGATCGGGGGCAGG  
TGTGGTGAACACAGTATCCATAGGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCAACTATGGGAGAATATTGATGACCAGGCCAAG  
GCTTAATTGGAAATCTCATGTAATGATTCAACCCCTGAAAAAACTTCAGAATCTAGCCTGGATATGAAGAAGA  
GCTTCTTCAGAGGTTGGCCTGGACAAATGGNGTCCCTCCAGAAACACCCACATTACCTGTTCTTGG  
GTAGCTTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAAGCTGGAGGGCTGGAGAAGGGGTTGATTCA  
TCAATGGCCAGAACCTGGACGTTACTGGAACATTGGACCCCAGAAGACGCTTACCTCCAGGTCCCTGGTGA  
GCAGCGGAATCAACCAGGTATCGTTTGAGGAGACGATGGCGGCCCTGCATTACAGTTACGGAAACCCCCC  
ACCTGGCAGGAACAGTACATTAAGTGAGCGTGGCACCCCTCTGCTGGTGCAGTGGAGACTGCCGCTC  
CTCTTGACCTGAAGCCTGGCTGCCCCACCCCTCACTGCAAAGCATTCTCTTAAGTAGCAACCTCAGGG  
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCCCTAACGCTGCAGGGAAAGGTGGGATGGCTCTGGGCC  
TGGCTTGTTGATGATGGCTTCTACAGCCCTGCTCTGTGCCAGGGCTGCGGCTGTCTAGGGTGGGAGC  
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAAGTGCAGAACACGTGCCCTGCACCGGACGTACAGCCC  
TGCAGCATCTGCTGGACTCAGCGTGTCTTGTGCTGGTCTGGGAGGCTTGGCACATCCCTCATGGCCCCAT  
TTTATCCCGAAATCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTGT  
CTTCCCTCACAAACCTCTGAGCCTCTTGGGATTCTGAAGGAACCTGGCGTGAAGAACATGTGACTTCCCT  
TCCCTCCACTCGCTGCTTCCACAGGGTGACAGGCTGGAGAACAGAAATCTCACCCCTGCGTCTTCC  
CAAGTTAGCAGGTGTCTGGTGTTCAGTGAGGAGGACATGTGAGTCCCTGGCAGAACGCCATGGCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAACAGGCCAGCTCACATGTGAGTCCCTGGCAGAACGCCATGGCCATGTCTGACATCC  
AGGGAGGAGGACAGAACAGGCCAGCTCACATGTGAGTCCCTGGCAGAACGCCATGGCCATGTCTGACATCCAGGG  
GGAGGACAGAACAGGCCAGCTCACATGTGAGTCCCTGGCAGAACGCCATGGCCATGTCTGACATCCAGGGAGGAGG  
ACAGAACAGGCCAGCTCAGTGGCCCCGCTCCACCCCCCACGCCGAACAGCAGGGCAGAGCAGGCCCTCTC  
GAAGTGTGTCAGTCCGATTTGAGCCTGTTCTGGGGCCAGGCCAACACCTGGCTTGGGACTGTCTG  
GTTGCAGTAAAGCTATAACCTTGAATCACAA

## **FIGURE 64**

MTTWSLRRR PART LG LLL VV LG FL VL RR LD WST LV PL RL R H R Q L GL Q AK G W N F M L E D S T F W  
I F G G S I H Y F R V P R E Y W R D R L L K M K A C G L N T L T T Y V P W N L H E P E R G K F D F S G N L D L E A F V L M A  
A E I G L W V I L R P G P Y I C S E M D L G G L P S W L L Q D P G M R L R T T Y K G F T E A V D L Y F D H L M S R V V P L Q  
Y K R G G P I I A V Q V E N E Y G S Y N K D P A Y M P Y V K A L E D R G I V E L L L T S D N K D G L S K G I V Q G V L A T  
I N L Q S T H E L Q L L T T F L F N V Q G T Q P K M V M E Y W T G W F D S W G G P H N I L D S S E V L K T V S A I V D A G S  
S I N L Y M F H G G T N F G F M N G A M H F H D Y K S D V T S Y D Y D A V L T E A G D Y T A K Y M K L R D F F G S I S G I P  
L P P P P D L L P K M P Y E P L T P V L Y L S L W D A L K Y L G E P I K S E K P I N M E N L P V N G G N G Q S F G Y I L Y E  
T S I T S S G I L S G H V H D R G Q V F V N T V S I G F L D Y K T T K I A V P L I Q G Y T V L R I L V E N R G R V N Y G E N  
I D D Q R K G L I G N L Y L N D S P L K N F R I Y S L D M K K S F F Q R F G L D K W X S L P E T P T L P A F F L G S L S I S  
S T P C D T F L K L E G W E K G V V F I N G Q N L G R Y W N I G P Q K T L Y L P G P W L S S G I N Q V I V F E E T M A G P A  
L Q F T E T P H L G R N Q Y I K

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## **FIGURE 65**

GGGGACCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGCTCGGCCGAGGCCCGAGGACCTCATCTCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAACGCTGTCCTGCCTCGTCCCTGCTGCGCTCAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTGCGTGTAGTGGATAGGGTCACTGACCGGTTCTCCTAGACGGGGCC  
CGTCCGCTATGTGTGGCAGCCTGCACTACTTCGGGTACCGCGGGTGCTTGGGCCGAC  
CGGCTTTGAAGATGCCATGGAGCGGCTCAACGCCATACAGTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGTCTCCATCCTGGTTGCTCGAAAACCTGAAATTCTAAGAACCTC  
AGATCCAGACTTCCCGCAGTGGACTCCTGGTTCAAGGTCTGCTGCCAAGATATATC  
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTTCCGTGACTGCTAGG  
AGAAAAGATCTGCTCTCACACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GAECTATACCACTGTAGATTTGGCCAGCTGACAACATGACCAAAATCTTACCTGCTT  
CGGAAGTATGAACCCCCATGGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGAGGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCCCTCCGATTACTACCAAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAACGTTAGCTTGTGAGATGTCATCAGCAAGT  
TCCAGGAAGTCCCTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTTGCTTGCCTGGCTGGACCTGT  
TCATTCAATCTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC  
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG  
AGACAAACTATTTTGACGGGAAACTGGGTCAAACACTGGATATCTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTGGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGTTAACATTGGGCCGGTACTGGACAAAGCAGGGCC  
ACAACAGACCTCTACGTGCCAAGATTCCCTGCTGTTCCATGGGAGCCCTAACAAAATTA  
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGGACTTGAAAGGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTAAACCCCCGTCTCCACTAAAAATACAAAATTAGCCGGCGTG  
ATGGTGGGCACCTCTAACATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAA

# FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGA SVNM MYMF HGGTNF  
GYWNGADKKGRFLPITT SYDYDAPISEAGDPTPKLFALRDVISKFQE VPPLGPLPPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## **FIGURE 67**

GCTTTGAACACGGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTC  
ACCCACAATATGGCTTACATGTTGAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT  
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAAGGAATATT  
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATT  
GCGTTCCCTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCAKGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGTGCCGATGCTGCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGCTAACGATTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTCTAGCTTCTCGCATCTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGATTGCTCAAAAA  
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCACATCTAACAAAGTTAGTCATTCTAACATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACCTGGAT  
TTAAAGTCCAATAACATTGCAACATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT  
GACTTGTAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA  
AAAACTTGGAGTCACTTATTCTCTAACAAACAAGCTCGAACCTTACCAAGTGGCAGTATT  
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAAATCTGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG  
TGGAAAGATCACCTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AACTTCTAGATTGCAAGTGCTACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGAGGGTTTAAGTCATTCAATTCAAATCATTGTTCTTTGGG  
AAAGGGAAAGGAAAATTATAACTAACTTGGTTCTTTAAATTGTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEI PAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAI FSLSNLQELDLKS  
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLES LPVAVFSLQ  
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## **FIGURE 69**

CCACCGCGTCCGGCCTCTCTGGACTTTGCATTCCATTCTTCAAGAAACTGACTTTTTATTTCT  
TTTTTCCATCTCTGGGCAGCTTGGGATCCTAGGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT  
CTGTGTTGGGTTCTTCCTCCCTGACATTGGCATTGCTTAGTGGTGTGGGGAGGGAGACACGTGG  
GCTCAGTGCTTGCTGCACTTATCTGCTTAGTACATCGAAGTCTTGACCTCCATACAGTATTGCTGTC  
ATCGCTGGTGGTATCCTGGCGCTTGCTCTGCTGATAGTGTGCTGCTGTCTTACTTCAAATACACAAC  
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGGCTGAAAAAATACAACCCAGACAAGGTGTGGTGGCCAAG  
AACAGCCAGGCCAAACCATGCCACGGAGTCTGCTGCCCTGAGTGTGAAGGATATAGAATGTGTGCC  
AGTTTGATTCCCTGCCACCTTGCTGCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA  
GCAGAGCCCTGAAGACTCAATGATGTCATGAGGCCACCTGTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGGACCAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGCAACCCCTCAGGAAGGAGTTGGGAGAGAGAACCCACTGTGGGAATGCTGATAAACCAAGTC  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGCTGAACTGACGTTCCCTGGAGGTGTCAGAAA  
GCTGATGTAACACAGAGCTATAAGCTGTCGGTCTTAAGGCTGCCAGGCCCTGCAAATGGAGCTTGTA  
AGAAGGCTCATGCCATTGACCCCTCTAATTCTCCTGTTGGGGAGCTGACATGGCGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCTAATGGCAGAGACCCACAAGGCATGATCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAAGACAGAAAACAAAGCATCAGAATTATCTTCTATGTCAGCTT  
GATCCAGATGGAAGCTGTTGAAAGTGAAAACATTAAAGTCTTGACGGAACCTCCAGCAATGGGCTCTGCTAGGG  
CAAGTCTGAGTAAAACACTATGTCCTGATTGAAACTCATCAGTCAGTACATTGACGTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAACTGTCTTGTCTACTACTCTTCTCTCTAACATCTCTATTCCAAACTGT  
GGCGTTACCTGGATACCTTGGAGGATCCTTCACCAGCCCAATTACCCAAAGCCGATCTGAGCTGGCTTAT  
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTCAAAGAGATTTCCTAGAAATAGAC  
AAACAGTGCACAAATTGATTTCCTGCCATCTATGATGGCCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT  
GGCGTGTGACTCCCACCTCGAATCGTCAACTCTGACTGTGTTGCTACAGATTATGCAATTCT  
TACCGGGGATTCTGCTTCTACACCTCAATTATGAGAAAACATCAACACTACATCTTAACTGCTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTAACTCTAATGGGAATAACTGCAACTAAA  
GACCCAACCTGAGACCAAAATTATCAAATGTTGGAATTCTGTCCTCTTAATGGATGTGGTACAATCAGA  
AAGGTAGAAGATCAGTCACCAATTACACCAATATAATCACCTTCTGCATCTCAACTCTGAAGTGTACCC  
CGTCAGAAACAACCTCCAGATTATGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACATAACA  
GAAGATGATGTAATACAAAGTCAAATGCACCTGGCAAATATAACACCCAGCATGGCTTTGAATCCAATTCA  
TTTGAAGACTATACTGAATCACCATTATGTTGATTGACCAAACCTCTTGTGTTCAAGTTAGTCTGCAC  
ACCTCAGATCCAAATTGGTGGTCTTGATACCTGTAGAGCCTCTCCACCTGACTTGCATCTCCAACC  
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTGTAAGGTGTATCCCTTATTGACACTATGGGAGA  
TTCCAGTTAACGCTTAAATTCTTGAGAAGTATGAGCTCTGTTGATCTGCAGTGTAAAGTTTGATATGTGAT  
AGCAGTGACCACCGACTCGCTGCAATCAAGGTGTGCTCCAGAAGCAGAGACATTCTTCTCATATAATGG  
AAAACAGATTCCATCATAGGACCCATTGCTGAAAGGATCGAAGTGCAGTGGCAATTCAAGGATTTCAGCAT  
GAAACACATGGGAAGAAACTCCAAACCCAGCCTTCAACAGTGTGCACTGTTCTCATGGTTCTAGCTCTG  
AATGTGGTGAATGTTGAGCACAATCACAGTGGCATTTGAAATCAACGGGAGACTACAAATACCAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCTAAGTGGAGACATGTTCTCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTATGAAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCCTGATGTA

## **FIGURE 70**

MELVRRLMPLTLLIISCLAE LTMAEAEGNASCTVSLGGANMAETHKAMILQLN PSENCTWTI  
ER PENKSIRIIFSYVQLDPDGSCES ENIKVFDGTSSNGPLLQVC SKNDYVPVFESSSTLT  
FQIVTDSARIQRTVVFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFL EIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSAS YTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDV IQSQNALGKYNTSMALFESNSFEKTI LESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFN AFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGC VSR SKRD ISSYKW KTD SII GPIRLKRDRSASGN SGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVT VATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGGAGCCTGCAGAGAGGACAGCCGGCTCGGCCG  
GGACATGCGGCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC  
TGCTGCCGCCGCCGTGCCCTGCCACAGGCCACGCCGCTCGACCCCACCTGGGAGTCC  
CTGGACGCCGCCAGCTGCCCGCTGGTTGACCAGGCCAAGTCGGCATCTCATCCACTG  
GGGAGTGTTCGCCCAGCTCGTAGCGAGTGGTCTGGTGTATTGGCAAAGGAAA  
AGATACCGAAGTATGGAATTATGAAAGATAATTACCCCTAGTTCAAATATGAAGAT  
TTTGGACCACTATTACAGAAAATTTTAATGCCAACAGTGGCAGATATTTCAGGC  
CTCTGGTGCAAATACATTGCTTAACCTCAAACATCATGAAGGCTTACCTTGTGGGGT  
CAGAATATTGTGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA  
ATGGTTTCACTCGCTTCCCTGAGGATGAATCCAGTTCACTCCATAAGCGGCAATTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACGGATCAAACTGGAACAGCACAGGCTTCTGGCCTGGTT  
ATATAATGAAAGCCCAGTTGGGGCACAGTAGTCACCAATGATGTTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTCTACCTGCAGTGATCGTTATAACCCAGGACATCTTGCCA  
CATAAATGGAAAAGTCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGAAAGCTGG  
AATCTCTGACTATCTACAATTGAAGAATTGGTAGAAGCAACTTGTAGAGACAGTTCATGTG  
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCCAGATGTGTTGACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTCCTAAATGGGCCACATCAGGACAGCTGTTCTGGCCAT  
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC TG  
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC  
CGTGTAAATGGGGCTGGCTAGCCCTAACTAATGTGATTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACGGATAAGAAAATTATTGGCAGTTAGCCCTTCCCTTTCCACTA  
AATTTTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTTGCCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGACCGAAGTGGAAATTCTGGGAAATGCATTGCTAGTCAT  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATGAAACATATGAAACATAGAGAAG  
GTACAGTAAAAAAACTGTAACGAAATGGTCACCTGTATAGGGCACTTACCAAGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTAAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAAA  
GTTTTCTTCTTCAATTATAAATTAAACATAAGTGTACTGTAACATTACAAACGTTTAATT  
TTTAAAACCTTTGGCTCTTGTAAATAACACTAGCTAAAACATAAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRIAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFIHWG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSPKPEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## **FIGURE 73**

## **FIGURE 74**

MARCFSLVLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVISRISPNNPKCGKNGVGVLIWKVPVRQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFTPNTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTTCGGTGCCCGACTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGCTGCCACCCAACGCGAAGACGTAACCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT  
TCTTTCTTCCGCTTGGATATTCGATGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACCTAGAACGGGACAAGAGGGTCACGGATTGTGGAGTTTTGCCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTTGGGAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC  
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGGCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACACAGTGTCAATT  
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCTGTCAATT  
CCAGGCTCTTCCATAACCACAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTG  
CTGNGACTGGNTGGGGCAGCAGCTGAGCTCTGATTAAAGAGGCATCTAGGAAATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGGCCAAGCTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTAACTGCTTATC  
AGCTATTGACAGCATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTCTTAG  
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTCCTTCAAGGACTCTGCTTCTTAAGCCCTCTGGCTTATGGTC  
TTCATTAAAAGTATAAGCCTAACCTTGTGCTAGTCCTAAAGGAGAAACCTTAACCACAAAG  
TTTTTATCATTGAAGACAATTGAACAACCCCTATTTGTGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTGGAGGAGAAATCCCTGGACTTCAC  
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRACKLSKAGDNIPPEEQPVASTPTTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## **FIGURE 77**

GGACAGCTCGCGCCCCCGAGAGCTTAGCCGTGAGGAGCTGCCTGGGACGTTGCCCTG  
GGGCCAGCCTGGCCGGTCACCCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCA  
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGGAGACCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCGCGCGTGTGCGTGTCAAATGGTGAAGCT  
GTCGGAGAACGGGCCAGAGAAGGACGTGCTGGCATCGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCGCGTGCACCTGCGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTCGGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGGCTGGAGCTGCGGGGTGTGGCTTTCCCTACCAGTCCCCCA  
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAAGAGCAGGCTGCCGTG  
GTGGCCTCCTTGAGCAGCTTCCGGCCTGGAGGAGGGCTGGACTGGTGCAACGCCGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCACATGTTGCCCGGCAGCCCTGCCGTGGCC  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACCGCCGCTGCACCGCTATGAT  
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC  
AGCTTTGCCGCTGGAAGTTCCATGGCCTGGACCGCTGCCACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCCTGTGGTTACCCGCATCTAACTGTGGCCCCCAGAGCCTGGGT  
CCGAAGCTTGGCTTCCCCGACCCGCAGAGCCGCTTGTACGGTGTACTGCTACCGCCAGC  
ACTAGGGACTGGGCCCTCCCGCCATTCCCTACTGGCTGTGTTAGTGGTGGTT  
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT  
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCCAAATGCCCTCCCTTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGCCATTGCGGTTGTGGCTCTG  
GAGGGTTCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCAGAGTGGC  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTTCTCCCTGCCCT  
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC  
CACCTCTACTCTGTGAAGCCGCTGACCCCAGTCTGCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTTCCAGGCAGAATCTGAGGGAAGGAAGAAACTCCCTCCCCGTTCCCT  
TCCCTCTCGGTTCAAAGAAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCTCCGCCAA  
AAA  
AAA

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYNSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ  
VCAEQAAVVVASFEQLFRAWEELDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVPVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

## **FIGURE 80**

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPISDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAAWVQTERQQ  
FRDFRDLNKGHDGHLGSVEGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## **FIGURE 81**

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGTGGATCTGAGCAGGTGCGGAGCCCCCG  
GCGGCCGGCGCGGGTGCAGGGATCCCTGACGCCCTGTCCTGTTCTTGTCGCTCCAG  
CCTGTCCTGTCGTTGGCGCCCCGCCCTCCCCCGCGTGCAGGGTTGCACACCGATCTG  
GGCTTCGCTCGATTGCCGCCAGGCGCCTCCCAGACCTAGAGGGCGCTGCCCTGGAGCAG  
CGGGTCGTCTGTCCTCTCCTCTGCCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT  
GAGGAGGTGACCGCGGGGCCTCCGCACCCCTGGCTTGCCTGCATTCCTCTCTCCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGCTCTGCCCTCGGTGTG  
TGTCTGCTGCTGCTGCCGGGCCGGCAGCAGGGAGCCGCTCCATTGCTATCACATG  
TTTACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC  
CTCTGAGGAATTCTCTGTATGGAACATAGTATATGCTTCTGTATCAGCATATGTGGG  
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTTCTTCACAGTAACAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGG  
CAATAAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTAAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA  
GAAGGACCACATGTGGCCTTGTCAAGCCAGTAAACATCCAAAATAGAATTACTGAA  
AAACTTACATCAGCCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT  
CGAGGAAGCAGGCATTGCGCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGCCA  
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT  
CGGAATAATGGCTTCTCTTACACATGCCAACTGGTTGGCACCAAAACAGTAAA  
GCCTCTGGTACAGAAGCTGTGCACCATGAACAAATGATGTGCAGCAAGACCTGTTAAACT  
CAGTGAACATTGCCCTTAATTGATGGCCAGCAGTGGAGATAGCAATTCCGCCCTC  
ATGCTGAAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCCTAAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCCACGGAGTTCAAGTTCAGTTCACTGACTATAGCACCA  
AAGAGAATGTCTTAGCTGTCACTCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT  
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGCAGTCCATGATGATGTCCTAGGCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTCTCTGTTGGTGTGGCTGGCACCTCTGGATGACCTG  
AAAGATATGGCTCTAAACCGAAGGAGTCTCACGCTTCTCACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTTAAATCCAGCAAT  
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGATCCAGTGTGAAATTGATT  
CTCATATACTGAAATGCTTACGACTAGAATCAGATAAAAATTAAGTATGTCAC  
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCAATCATGGCTCTTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCAACCAGCCTACTAAATGTACAGATATGCAA  
TTCCATAGCTCAAAAAGAATCTGATACTTAGACCAAAAAAAA

## **FIGURE 82**

MSAAWI PALGLGVCLLLLPGPAGSEGA APIA ITCFTRGLDIRKE KADVLCPGGC PLEEF SVY  
GNIVYASVSSICGAAVHRGVISNSGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDC KADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNNGFFSYHMPNWF GTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRLMLEFVSNIAKT F EISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQS YDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## **FIGURE 83**

CGCCCGCGCTCCGCACCCGGGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC  
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG  
GGGCGGCGGCTCGGGCGCAGAGCGGAGAT**G**CAGCGGCTGGGGCACCCCTGCTGTGCCTGC  
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCGGCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCTCAATGAGATGTTCCCGGA  
GGTTGAGGAACGTGATGGAGGACACGCAGCACAAATTGCGCAGCGGGTGGAAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTAT  
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC  
ATGTAATGCCAGTTGCCAGCTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA  
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACACCAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTTCCAGAGAGGGCTGCTGTTCCCTGTGTCACACCCCTGCCGTGGAGGGCGA  
GCTTGCCATGACCCGCCAGCCGGCTTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCCTGTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTCATGGAGGAGGTGCCAGGAGCTGG  
AGGACCTGGAGAGGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGGTGCCTGCCGCT  
GCACTGCTGGGAGGGAAAGAGATT**TAGAT**CTGGACCAAGGCTGTGGTAGATGTGCAATAGAA  
ATAGCTAATTATTCCCCAGGTGTGCTTGTGACAGCTGGCTCTGGCTGACAGGCTTCTTCTACA  
TCTTCTTCCCAGTAAGTTCCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTCAGC  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTTGGGAGAGTCAGGCAGGGTAAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATGGCTGCTTGCCTCTACCAGTTGGCAG  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGGAGGAGATGGAACAAATGTGG  
AGTCTCCCTCTGATTGGTTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAACATCAA  
CCTGGCAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCTGCATTACATGTGTTATTGATCC  
AGCAGTGTGCTCAGCTCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT  
CCTCTCTCAGCACAGCCTGGGAGGGGTATTGTTCTCCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCAT  
CTGGTTGTGACTCTAACGCTCAGTGCTCTCCACTACCCACACCAGCCTGGTGCACCAA  
AAAGTGTCCCCAAAAGGAAGGAGAATGGGATTTCTTGAGGCATGCACATCTGGAATTAAG  
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
AGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTGGCAGT  
TGCATTAGTAACATTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAACACTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTGATCCAGAGTTCTTAAAGTTAAAGTGCACATGATTGTA  
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC  
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGGLCAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPEYEV  
GSFMEEVROELEDLERSLTEEMALGEPAAAAALLGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

AAGGAGGGCTGGGAGGAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTTCAGCCCCATCCACTCTCCTTCCCTCAAACACACATGTGCATGTACACACACACATACA  
CACACATACACCTTCCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC  
TAAAGGCCCTAAGGACAGGCCATTACCTCTGCAGCTCCTTGGCTTGTGAGTCAAAAACATGGGAGGG  
CCAGGCACGGTGAECTCACACCTGTAATCCCAGCATTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTAGGG  
TTCGAGACCAGCTGGCCAACATGGAGAAACCCCCATCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC  
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGATCGCTGAATCCAGGAGGCGGAGGATGCAGT  
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTAAACAAACAAACACGGGAGGA  
GGGGTAGATACTGCTTCTGCAACCTCTTAACCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCCCTG  
GCAATGACTGAGCAGGCCAGGCCAGAGGACAAGGAAGAGCATATTGAGGAGGGCAAGAAGTGA  
GCCCCG  
GTGTTAGAATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGGCAGGGTGTGACCCCTTACCTGCAAAACACA  
AAGAGCAGGACTCCAGACTCTCTTGTAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC  
ACTCTGCTAGCTTGGGTGGCTGGCAGTGCCTACTGTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCC  
GTGTCCTGCCAGATCCGGGCTGGTATAACGCCCGCTCGTCTTACCGCCAGGCTACCAACTGTGGACTGCAATGA  
CCTATTCTGACGGCAGTCCCCCGCACTCCCCCGCAGGCCACAGACAGCTCCTGCAGAGCAACAGCATTGT  
CCGTGTGGACAGACTGTGAGCTGGGCTACCTGGGCAATCTCAGAGCTGGACCTGGTACCCCTGGCATGTTCC  
TGCCCGAGACTGTGATTCATGCCCTGCCCTGGGAGATCTGCTGAGCCTAGAGGAGAACAGCTGACCCGG  
GGAGGACACAGCTTGAGGGCTGGCAGGCCACAGGAACCTCTATCTCAACACCACACAGCTTACCCGATCGC  
CCCCAGGGCTTTCTGGCCTCAGCAACTTGCTGCCCTGACCTCAACTCCAAACCTCTGAGGGCCATTGACAG  
CCGCTGGTTGAAATGCTGCCCAACTGGAGATACTCATGATTGGCGCAACAAGTAGATGCCATTGGACAT  
GAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTGTAGCAGGCAACCTGCCGGAGATCTCGACTATGC  
CCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCTATGACAACAGCTGCCGGGTGCCAGCGGGCACT  
GGAACAGGTGCCCGGCTCAAGTTCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTG  
CAACATGCTGCACCTTAAGGAGCTGGACTGAACAAACATGGAGGAGCTGGTCTCATCGACAAGTTGCC  
GAACCTCCCCGAGCTGACCAAGCTGGACATCCAATAACCCACGGCTGTCTCATCCACCCCCCGCGC  
CCACCTGCCAGATGGAGACCCCTATGCTCAACAAACAGCTCTCAGTGCCTTGCAACCAGACGGTGGAGTC  
CCTGCCAACCTGCAAGGAGGTAGGTCTCACGGCAACCCATCCGCTGTGACTGTGTCATCCGCTGG  
CACGGCACCCGTGTCCGCTTCATCGAGCGCAATCCACCCGTGTGCGGAGCCTCCAGCGCCTCCC  
GGTCCGTGAGGTGCCCTCCGGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACGAAGCTTCCCC  
CCTCCAGGTAGCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGCCGAACCCGAACCGAGATCTACTG  
GGTCACTCCAGCTGGCTTGCACTGACACCTGCCATGCAGGCAGGAGGTACCGGGTGTACCCGAGGG  
GGAGCTGCGGAGGGTGACACAGAGGAGGCCAGGGTATACACCTGTGTTGGCCAGAACCTGGTGGGG  
TAAGACGGTTAGTGTGGTTGTCGGCTCTCCAGCCAGGCGAGGAAGGGACAGGGCTGGAGCTCG  
GGTGCAGGAGACCCCTATCACATCCTGCTATCTGGGTCAACCCACCCAACAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCTCCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCCTGCCCTGGGAACCCACAGCTA  
CAACATTACCCGCCCTTCAGGCCACGGAGTACTGGCCTGCCATGCAAGTGGCTTGCTGATGCC  
GTTGGCTGTGATGGCCAGGACCAAAGAGGCCACTTCTGCCACAGAGCCTTAGGGATGTC  
TGCCATCCTGGCTCTGCTGCTCTCTGGCAGCTGGCTAGCGGCCACCTGGCACAGGCCACCC  
GGGTGTGGGTGGAGGGCGGCCCTCCGCCAGGCCGGCTTCTGGGCTGGAGTGCCCTTCTGTCC  
GTCTGCTCCCTCGTCCCTGCCCTGGAAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAG  
ACACTGTTGCC  
ACCATTGTCTAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACT  
AGAGAACAGTCTGGGCCAGATGCCCTGCCAGGAAGGGACATGGACCCACGTGCTTGAGGCC  
CAAGACAGATGGGTTTGTCGGCTGGGGTGTCTGCCAGCCTGGTAAAAAGTTGCCCTAAC  
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCTGCC  
CTCTCTGCCAGAGGCTCTGGGCCCTGGCTTGTCTGCCCTACCTGTGTC  
TCTTCTCTGTACAGTCTCAGTTGCTTGTGCTCTGCCCTGGCAAGGGCTGAAGGAGGCC  
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGA  
CGCCTCATCTCAGCAGCCTGGCTCGGCATTCCGAAGCTGACTTCTATAGG  
ATGTGTCA  
ATTTGTGACCTCCCCAACCCGATTCACTCTTCTCCTGTTGAAAA  
AAAA  
AAAA

## **FIGURE 86**

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQEYLHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLRREISDYALEGLQSLSFYDNQ  
LARVPRRALEQVPGLKFLDLNKPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHHLQPQMELMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVALLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGWSAPSVRVV  
SAPLVLPWNPGRKLPRSSGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## FIGURE 87

## FIGURE 88

MRQTIIKVIKFILIICTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQLNLLNEWTLDKLQRQLTKNAQDKLELHLFMLSGLPDTVFDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRALHLGNNVLQSLPSRVGELETNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGGTGTGATGCCGTGGTACTTGTCAATGGAGCTGGCACTGCGGCCCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTATTGACT  
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC  
CCCTTGACAGTGTCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT  
GTGGATAATCCCGTGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG  
AATTCCAGACAGTCCATTCTACATTTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGCAGGGGGT  
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGACCTTACCTGT  
ACAGCATGTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTGTCTTGTAGCGC  
CACGTGAGACACCTACAACGAGATGCCCTAAGCCAGCTCATGAATGCCCATCAGAAAGAA  
GCTAAAATTATTCCCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCCTG  
GGTGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT  
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCAATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGTCACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
GGGGCACAGAGCTGAGCTGAGGCCGTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT  
AACTGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAACCTAAGATTTTAAAAATTGAT  
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLPLLLGLNAGAVIDWPTEEGKEWWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE  
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCCGCGCTTATCAGGACCATGCGCCGA  
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCA**CTCGGGCGTGGCGTGGCA**  
GGGGAGCCTGCGCCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCCTGGG  
CACTCACGGCGGCGCACTGCTTGAAACCTATA**GTGACCTTAGTGATCCCTCCGGTGGATG**  
**GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG**  
**TTACTTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGGATTCAACCTATGACATTG**  
CCTTGGTGAAGCTGTCTGCACCTGTACCTACACTAAACACATCCAGCCC**ATCTGTCTCCAG**  
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAAACAA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGGCAACGCCAACGGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGCCCAATCGGCCGGTGTACACCAATATCAGCCACC**ACTTGTGGATCCAGAAG**  
CTGATGGCCCAAGACTGGCATGTCCCAGCCAGACCCCTCTGGCC**ACTACTCTTTCCCTCT**  
TCTCTGGCTCTCCACTCCTGGGCCGGTCT**TGA**GCCTACCTGAGCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTCTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLALLLARAGLRKPEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCVGVSLLSHRWALTAAHCFETYSDLSDPGWMQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVGCGRPGRPVGVTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCCCACCGCTCCGGAGCGTGGGAAGGGCAGAATGGACTCCAAGCCTGCCTCCTAGGGCT  
CTTTGCCCTCATCCTCTGGCAAATGCAGTTACAGGCCGGAGCCCACCAGCGGAGGACGC  
TGCCCCCAGGCTGGGTGCCCCCTGGCCGTGGGACCCCTGAGGAAGAGCTGAGTCTCACCTT  
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG  
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGGGCCATCCC  
CACTGACCCCTCACCGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCCTTCT  
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTCATCACTATGTGGAGGACCTACGAAACCCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTGTGGGGGACTGCACCGT  
TTTCCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGTAACCCCTCTGTATCCGTAAGCGATAACAACCTGACCTCACAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCTGGAGCAGTATTCCATGAC  
TCAGACCTGGCTCAGTTCATGCCCTCTCGGTGGCAACTTGCACATCAGGCATCAGTAGC  
CCGTGTGGTTGACAACAGGGCGGGCCGGGCGGGATTGAGGCCAGTCTAGATGTGAGT  
ACCTGATGAGTGTGGTGCACACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTCCTGCAGTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGAGGACTCCCTCAGCAGGCCACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT  
GGGGCCGGGTGGTGTCTGTCTCTGGAAAGACACCAGTCCGCCCTACCTTCCCTGCCCTCAG  
CCCCTATGTCACCACAGTGGGAGGCACATCCTCCAGGAACCTTCCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGTGGTCAGCAACA  
GAGTGCCCATCCATGGGTGTCCGGAACCTCGCCCTACTCCAGTGTGTTGGGGGATCTA  
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCCCCCCTCTGGCTTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGGCAGGTCTTTGATGTAACCGTGGCTGCCATGAGTCCGTGTC  
TGGATGAAGAGGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGATCTGTAACAGGC  
GGGGAAACACCAACTTCCAGCTTGCTGAAGACTCTACTCAACCCCTGACCCTTCTATC  
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCTGAAA  
TGCTGTGAGCTTGACTTCACTCCAAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTAGATTCCCTCAATAAGATGCTGTAACTAGCATTGGATGCTCTCCCTCCGC  
ATCTCATCTTCTTTCAATCAGGCTTCCAAAGGGTGTATAACAGACTCTGTGCACTA  
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTACTGTCACCGTTACTCT  
TTCCACTCCAGATCCAGAAACAAATGGCCTCCAGTGCATACTTCTCAATCTTGTGTTATG  
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTTCCAGGTCTTAACCTCTG  
ACTACTCTGTCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC  
TCCATTGAGATTGGCTCTCAGTTACTCATTGTCACCGTTACTCAATGACCAAAACTGACA  
TCTACAAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATACTCAAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGYLTLENVALVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSCTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## **FIGURE 95**

GCCGCGCGCTCTCTCCC GGCGCCACACCTGTCTGAGCGCGCAGCGAGCCGGCCCCGGGC  
GGGCTGCTCGCGCGGAACAGTGCTCGCATGGCAGGGATTCCAGGGCTCCTCTTCTC  
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTAACAGTGCCCTGGAAACCCACTTG  
GCCTGCATACCGCCTCCCTGTCGTCTGCCCAAGTCTACCCCTAACCTAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTAAGGGAAC  
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCAAAC  
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGCACCCCTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTTCTAAAGCCC  
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA  
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACCTCAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGGCAGAATTCACTTCTC  
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGGGCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGAGCGAAAAATTATTGGCATTTCAGG  
GCACCAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAACACTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG  
TGACACAGTGGTCCCTCTGGCAGCAATTAAAGGTCTTCTATGTTCTTATTAGGAGAGGCC  
AAATTGTTTTGTCTTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG  
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAAAGTTAATCTCACGTTTG  
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATTTGGCATA  
CAAGAGATATGAAAAAAAAAAAAAA

## **FIGURE 96**

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLHQSTLNLAQPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDGSQGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAACIHDGKTYVKG  
TQKLRVGFLKPQFKDGGRGANDSTSAMPQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLQQCD  
AQPGASGSGVYVRMWKRQQQWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## **FIGURE 97**

GCATGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTT  
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAAGCCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCCTGGGTGGAGC  
CCCACCCCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCATCTGCCTACCTGATGCCCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGTTGCTGGCGACTCCGGGGCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCGGCATCATCAGCTGGGCGAGGGCTGTGCCGAGCGCAACAGGCC  
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGTGAGAAGATCGTCAAGGGGTGCA  
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC  
CCCGCGCTCCTAGGGCGCAGCGGGACGCAGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGCGGCCTCGGGCGTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCTGCGAAAGGAAACCCCTCCCCGACCGCCCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAC  
GACTTCCGGCCCCGCCGGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTTTAT  
AGGTATTTGTAACCTGCCACATATCTTATTTATTCTCCAATTCAATAAATTATTATT  
CTCCAAAAAAA

## **FIGURE 98**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAACFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGII SWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAAGACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC  
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTCGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCAGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAAC TGAGGCCCATCCTTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGATTCCGGCTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC  
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTAAC  
AACTGAGGTCCCTTCCATTTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCCATCCAAAATCAGCAGACAAAGTGAAGACAAAAACA  
AAAGTGCCTCTAGGAGCCCAGAGAACTCTGGACCCCAAGATGTCCCTGACAGGGCAAG  
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGTGAGCTGCAGGCCACACTGGAC  
AGGTCTTGCCTCAGTTTCCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGCTGCCAGGTGCAGAGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCTGGGA  
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACCTAAAGGG  
TGAAGAGGTCAGCTGCCTCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCTGCCCTCCCTGGCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTCCTG  
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC  
TTGAGTGGGGAGGCAGGGACGAGGAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVDPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPYLVTTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSPLSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## FIGURE 101

GTAAGTGAAGTCAGGCTTTCAATTGGGAAGCCCCCTCAACAGAATTGGTCATTCTCCAAGTTATGGTGGACGT  
ACTTCTGTTGTTCTCCCTCTGCTTGCTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTCAT  
CAAGGCAGTTCCATGAGCACCTTCAAAGCCTCGAGAAGTGAAGACTGAACAACAATGAATTGGAGACCATTCC  
AAATCTGGGACCAAGTCTCGCAAATATTACACTCTCTCCTGGCTGAAACAGGATTGGAAATACTCCCTGA  
ACATCTGAAAGAGTTTCAGTCCCTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAA  
TTTGGCCAACACACTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACT  
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTTAGATGGACTGACATTCCAAGGCCTGG  
TGCTCTGAAGTCTCTGAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA  
CATGAAATTTCAGCAGCTAACACACTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT  
GCAGGAACCTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAACTTCAATCACTTCAAGGTTAGATGATTCAAGCTTCTGGCTAAGCTTACTAAATAC  
ACTGCACATTGGGAACACAGAGTCAGCTACATTGCTGATTGTGCCTCCGGGGCTTCCAGTTAAAGACTTT  
GGATCTGAAGAACAAATGAAATTCTGGACTATTGAAGACATGAATGGTGTCTCTGGCTTGACAAACTGAG  
GCGACTGATACTCCAAGGAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCA  
TCTAGACCTGAGTGAACACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATT  
GCATTAAATACATCAAGCCTTGTGCAGTGGCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACCTT  
TCAGAGCTTGTAAATGCCAGTTGTGCCATCCTCAGCTGCTAAAAGGAAGAACGATTGGCTGTTAGCCAGA  
TGGCTTGTGTGATGATTTCCAAACCCAGATCACGGTTCAGGCCAGAAACACAGTCGCAATAAAAGGTT  
CAATTGAGTTCATCTGTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTGTGCTTGGAAAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCCAAGGTGGCAGGATGATGGAGTATACCAC  
CATCCTCGGCTGCGAGGTGGAATTGCCAGTGAGGGAAAATATCAGTGTGTCATCTCAAATCATTGGTT  
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATCACCAAGACCCCCATGGATCTCACC  
CCGAGCTGGGGCCATGGCACGCTGGAGTGCTGCTGTGGGGCACCCAGATAGCCTGGCAGAACG  
TGGGGCACAGACTCCAGCTGCACGGAGAGACGCATGCTGATGGCAGGATGACGTGTTCTTATCGT  
GGATGTGAAGAGTAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTCAGCAAATGC  
AACTCTGACTGTCCTAGAACACCATCATTTCAGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAACAGC  
CGTCTTACAGTGCAATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATAGCCATTGGT  
AACCGAGAGGCACTTTGTGAGCAGGCAATCAGCTCTGATTATTGTGACTCAGATGTCAGTGTGCTGGGAA  
ATACACATGTGAGATGTCACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC  
CTGCACTCCCCCTCAGATGACAGCCCCATCGTAGACGATGACGGATGGCCACTGTGGTGTGTCATAGC  
CGTGGTTGCTGTGTGGCACGTCACTCGTGTGGTGGTCACTCATATACCACACAAGGCGGAGGAATGAAGA  
TTGCACTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTCACTCAGGGAAACGTT  
AGCTGACAGGCAGGATGGTACGTGCTTCAGAAAGTGGAAAGCCACACCAGTTGTACATCTCAGGTGCTGG  
ATTTTCTTACACACATGACAGTAGTGGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC  
CACAGATCTGTCCTTGTCCGTTGGATCCACAGGCCATGTTGAAAGGAAATGTGTATGGCTCAGA  
TCCTTTGAAACATATCATACAGGTGCACTGCAGTCTGACCCAAAGAACAGTTTAATGGACCACTATGAGCC  
CATAAAGAAAAGGAGTGTACCCATGTTCTCATCTTCAGAAAGAACCTGCAAGCAGCTTCAAGTAAATATC  
GTGGCCTTCACATGTGAGGAAGCTTAACACTAGTTCTCACAATGAAGGACCTGGAAATGAAAATCTGTG  
TCTAAACAAGTCCTCTTAGTTAGTGTCAAACTCAGAGGACCTCACCTAGATGCTTATTCAAGCTTGG  
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCTTATTCAAGCTTGGACAGCC  
AAGAGCCTTTATTGAAAGCTATTCTTCCCCAGACTGGACTCTGGTCAAGAGGAAGATGGAAAGAAAGGAC  
AGATTTCAAGGAGAAAATCACATTGTACCTTAAACAGACTTAAAGGAAACTACAGGACTCCAAATTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAGCTTAACACTACCTCAAGTGAACTTTATT  
AAAGAGAGAGAATCTTATGTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGAT  
GAACCAAATTACAAAAAGTATGAAAATTITATACTGGGAATGATGCTCATATAAGAATACCTTTAAACTA  
TTTTTAACTTGTGTTATGCAAAAAGTATCTACGTAATTAAATGATATAAATCATGATTATTTATGTATT  
TTATAATGCCAGATTCTTATGAAAATGAGTTACTAAAGCATTTAAATAACCTGCCTGTACCAATT  
TTAAATAGAAGTTACTTCATTATATTGACATTATTTAATAAAATGTGTCATTGAA

## **FIGURE 102**

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRIASAIPPKMFKLPQLQHLELRNKKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGMLQELHLSQNAINRISPDAWE  
FCQKLSLELDLTFNHLSRLDDSSFLGLSLLNLTIGHGNRVSYIADCAFRLSSLKTLIDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILOQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNFSFVNASCAPQLLKGRSIFAVSPDFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSDSPMTFAWKKDNELLHDAEMENYAHLRAQG  
GEVMETYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPKLNWTKDDSPVVTER  
HFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQM TAPS LDDDG  
WATVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNL PADI PSYLSSQGT LAD  
RQDGYVSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP  
MYLKGNVYGSDPFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCRSF SNISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLENY RTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 103**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTGGTGGTGGCTGGCTGGGCCTTGCAAAAATG  
AAGGATGCAGGACGCAGCTTCCTGGAACGCAACGCAATGGATAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCGGGGGGTGGTGTGTTCTGACATAATAATCTAAAGCAGCTGTTCCCCTCC  
CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACGAGGATTCAAAGAAAAAGTATGTTCATTTCTC  
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTGGAATGAAAAGTTGGGGCTTTTAGTAAAGTAAGAAACT  
GGTGTGGTGGTGTTCCTTCTTTGAAATTCCCACAAGAGGAGAGGAAATTATAATACATCTGCAAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCACAGTGG  
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCACTGGATTTCATCAACCTCTTTTTAAAT  
TTTATTCCCTTGGTATCAAGATCATGCGTTCTCTGTTCTAACACCTGGATTTCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAACAGGACCAACACCAGATAAAATTATGAATGTTGAACAGAT  
GACCTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGT  
GCTGGCTCTCAACTCTTGTGGTGGCTGGTCTGGTGCAGACCTGCCCTCTGTGTGCTCTGCAGCAA  
CCAGITCAGCAAGGTGATTGTGTCGGAAAAACCTGCGTGGGATGGCATCTCCACCAACACACGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCCTCAAGCAGCTGAGGCACTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGCTTCATGGTCTGGCAACCTAACACTCTGGA  
ACTCTTGACAATCGTCTTACTACCATCCGAATTGGAGCTTTGTATACTTGCTAAACTGAAGGAGCTGGTT  
GCGAACAAACCCATTGAAAGCATCCCTCTTACAGAATTCCCTTGTGACACCTGGCACACAATAATCTAAC  
GGAATTGAAAAGACTTTCATACATCTCAGAACGGCTTGAAGGTCTGTCCAACCTGAGGTATTGAAACCTTGC  
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAAGTGAACAGCCTGAGGATCTCTGGAAATCA  
TTTATCTGCCATAGGCCCTGGCTCTTCCAGGGTTGATGACACCTTCAAAACTGTGGATGATACAGTCCAGAT  
TCAAGTGATTGAAACGAATGCCTTGACAACCTTCACTGACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTCTTCACTCCCTGCATCATCTAGAGCGGATACATTACATCACACACCCCTGGAACTG  
TAACGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCGGTG  
TAACACTCCTCCAACTCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAACATTACTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTGGGCTCACATC  
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGCGTACAAAGTGCAGGATAGCTGT  
GCTCAGTGTGGTACGTTAAATTCAAAATGTAACGTGCAAGATAACAGGCATGTACACATGTATGGTGGTAA  
TTCCTGGGAAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAAGAACCAACTACTCCTTCTTACTTTTCA  
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCACTCC  
AGTGGTCAGTGGAGACCACCAATGTGACCACCTCTCACACCACAGGACAAAGGTGACAGAGAAAACCTT  
CACCACCCAGTGACTGATATAAACAGTGGGATCCAGGAATTGATGAGGTCTGAAGAGACTACCAAAATCATCAT  
TGGGTGTTTGTGGCATCACACTCATGGCTGCAGTGTGCTGGTCAATTCTACAAGATGAGGAAGCAGCACCA  
CTGGCAAAACCATCACGCCAACAAGGACTGTTGAAATTATAATGTGGATGATGAGATTACGGGAGACACACC  
CATGGAAAAGCCACCTGCCCATGCCGTATCGAGCATGAGCACCTAAACTACATAACTCATACAAATCTCCCTT  
CAACACACAAACAGTTAACACAAATAAAATTCAATACACAGTTCACTGCAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAAACAAACAATCAAAAAAA  
GACAGTTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA  
AAAAGAAAAGAAATTATTATTAAATTCTATTGTGATCTAAAGCAGACAAAAAA

## FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLLRRLDGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDLSGNHLSAIRPGSFQGLMHQQL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPLHHLERIHLHHNPWNCDIL  
WLSWWIKDMASTSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE  
LKCRASTSLTSVSWITPNGTVMTGAYKVRIAVLSDGTLNFTNVQDTGMYTCMVSNSVGN  
TTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYN SYKSPFNHTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## **FIGURE 105**

## **FIGURE 106**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGPSPGVAAPERCPPTCRLGDLLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLLKLNRRNRIASAIPPKMFKLPOLOHLELNRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMGAFWGGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDWEFC  
QKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLSDLKNNEIS  
WTIEDMNGAFSGLDKLRRRLILQGNRIRISITKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQLHLNTSSLLCDCQLKWLPQWVAENNQSFVNASCAPQOLLKGRSIFAVSPDGFVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTNVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAQIAWQKDGGTDFPAAREERRMHVMPEDDVFFIVDVKIEDIGVYSCAQNSA  
GSISANATLTVLETPSFLRPLLDRVTKGTAVALQCIAGGSPPPQLNWTKDDSPLVVTERHF  
FAAGNQLLIIVSDVDAGKYCEMSNTLGTERGNVRLSVIPTPTCDSPQMGTAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTIADRQ  
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGPMY  
LKGNVYGSDFETYHTGCPDPRTVLMHDYEPSYIKKKECYPCHSEESCERSFSNISWPS  
HVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLDSGSEEDKERTDFQEENHICTFKQTLNEYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## **FIGURE 107**

CAAAACTTGCCTCGCGGAGAGCGCCCAGTTGACTTGAATGGAAGGAGCCCGAGCCCGCGAGCGCAGCTGAGAC  
TGGGGAGCGCGTTCGGCCGTGCCCCGCGCTCGGCCGGGGCGCAGCAGGGAGGGAAAGCTGTGGTCTGCC  
CTGCTCCACGAGGCCTGAGCTGGTGTGAACCGGGAGAGCCCCCTGGGTGGTCCCTATCCCTCTTATATA  
GAAACCTTCCACACTGGAAAGGAGCAGCGCGAGGAGGAGGCTCATGGTGAAGCAAGGAGGCCGCTGATCTGCAG  
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAATGGAGGCAGGAGGAGGAGAAGCAGCTGCCGTGGT  
TCCATCAGCCCTGGCGCCAGCGCAGTCAGCTGCCACCCCTGCAGGCACCAGGCCAGAGGCCGGTCTGC  
TGCTCCTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTTGCCTGAGGGCCAGGATTGGCCGAA  
GTGGGGCCACGCCCTGAGGGCCAGAGAACGAATTGGCCAGGAGGAGGCCGTGCTGGTACTGAGGCCCTGAGG  
AGCCCCGGCTGGCCAGCCGGTCACTGCCCCCGAGACTGTGCTGCTTCCAGGGGCTCGTGGACTGTG  
GCGGTATTGACCTGCGTGAAGTCCCGGGGACCTGCCTGAGCACACCAACCTATCTCTGCAGAACACCAGC  
TGGAAAAGATCTACCTGAGGAGCTCTCCGGCTGCACCGGGTGGAGACACTGAAACCTGCAAACAAACCGCTGA  
CTTCCCAGGGCTCCAGAGAAGGCTTGTAGCATCTGACCAACCTCAATTACCTGACTTGCCAATAACAAGC  
TGACCTTGGCACCCGCTTCTGCAAACGCCGTGATCAGTGTGACTTGCTGCAACTATCTACCAAGATCT  
ATGGGCTCACCTTGGCCAGAACGCAAACCTGAGGTCTGTGACCTGACAACAAACAGCTGGCAGACGCCGGC  
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCAGCAACTTCTGCGCCACGTGC  
CCAAGCACCTGCCCTGCCCTGTACAAGCTGCAACCTCAAGAACACAAGCTGGAGAAGATCCCCCGGGGCCT  
TCAGCGAGCTGAGCAGCTGCCAGCTATACTGAGAACAAACTACCTGACTGACGAGGGCTGGACAACGAGA  
CCTTCTGGAAGCTCTCAGCCGGAGTACCTGGATCTGTCAGCAACAAACCTGTCAGGCCAGCTGGCTGC  
CGCGCAGCCTGGTCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGGACGCCAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGCTGTCAGCAACCGAGCTGCCGGAGCAGGGCATCCACCCACTGGCTTCCAGGGCC  
TCAAGCGGTTGACACGGTGCACCTGTACAACAAACGCGCTGGAGCGCTGCCAGTGGCTGCCGCGTGC  
GCACCCCTCATGATCCTGACAACCGAGTACAGGCATTGGCGCGAAGACTTGGCACCACCTACTTCTGGAGG  
AGCTCAACCTCAGCTACAACCGCATCACCAGGCCACAGGTGCACCGCGACGCCCTCCGCAAGCTGCGCTGCTGC  
GCTCGCTGGACCTGTCGGCAACCGGGCTGCACACCGTGCACCTGGCTGCGCTCGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCTGGCAGGAGGGGGCTGGCGGGCATGGCTCAGCTGCGTGAAGCTGTAACCTCA  
CCAGCAACCGACTGCCAGGCCAGCCCTGGGCCCCGGTGGCTGGGACCTGCCCATCTGCGAGCTGCTGGACA  
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCGAGTCACTTGAGTACCTGTCAGAACAAACA  
AGATTAGTGCAGGTCGGCTGGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAAGGTTAACAAAGC  
TGGCTGTGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAAGGTTGGACATTGAAGGCAACT  
TAGAGTTGGTGAACATTCCAAGGACCGTGGCCGCTTGGGAAGGGAAAGGAGGAGGAGGAAGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGAGATGTGACCTAGGATGATGGACCGCCGACTTTCTGC  
AGCACACGCCGTGCTGTGAGCCCCCACTCTGCCGTGTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCCACGGCCAGACACATGC  
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACAAACTACCCCTCAAACACCCACAGTCTGTCACAC  
CCCCACTACCGCTGCCACGCCCTCTGAATCATGAGGGAGGGCTGCCCTGCCAGCACACAGGCCACCA  
TTCCCTCCCCCTGCTGACATGTGATGCGTATGCATACACACCACACACACATGCAAGTCATGTGCGAA  
CAGCCCTCAAAGCCTATGCCACAGACAGCTTGCCTGCCAGGAGAATGCCATAGCAGCTGCCGTGCGCC  
GTCCCATCTGCCGTCCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTGTGCCAGGTGCCCTGCCACCCCT  
GGAACCTCACAAAAGCTGGCTTTATTCCCTTCCATCCTATGGGAGGGAGCCTCAGGACTGCTGGCCCTGGCC  
TGGCCCACCCCTGCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTCCAATGGGCAAGCCCAGTGGAGGAGGAGGAGGAGGCCCTGGGTGCTGCTGGGGCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT  
GTTCTCAGGCCGTGGGGAGTCCGGGTGCCCTTATTCTTATTCTTCTAAGGAAAAAAATGATAAAAAT  
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENFAEEEPLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETLNQNNRLLTSRGLPEKAFFEHTNLNYLYLANNK  
LT LAPRFLPNALISVDFAANYLT KIYGLTFQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EV LILSSNFLRHPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ET FWKLSSLEYLDLSSNNLSRVPA GLP RSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITS PQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA  
RGALAGMAQLRELYLTSNRRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANA FDSTPNLKGIFLRFNKLAVGSVVDSA FRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## **FIGURE 109**

GGGAGGGGGCTCCGGCGCGCAGCAGACCTGCTCCGGCGCGCCTCGCCGTGTCCTCCGGGAGCGGCAG  
CAGTAGCCGGCGGGCAGGGCTGGGGTCTCGAGACTCTCAGAGGGCGCCTCCATCGCGCCCACCACCC  
CAACCTGTTCTCGCGGCCACTGCCTGCAGCCAGGACCGCTGCCAAC**ATG**GATTTCCTGGCGCTGGT  
GCTGGTATCCTCGCTCACCTGCAGGGCGCGAGTCGACAGGGAGGTGGCCAGGAAATAGTGTATCGAT  
TGGCCTATGCGTTATGGTGGGAGGATTGACTGCTGGGCTGGCGCCAGTCTGGGACAGTGTCAAGCC  
TGTGTGCCAACACGATGCAAACATGGTAATGTATCGGGCAAAACAAGTGCAAGTGTCACTCTGGTTATGCTGG  
AAAAACCTGTAATCAAGATCTAAATGACTGTGGCTGAAGGCCGGCCCTGTAAGCACAGGTGCAACACTTA  
CGGCAGCTACAAGTGTCACTGTCTCACCGATATATGCTCATGCCGGATGGTCTGCTCAAGTGCCCTGACCTG  
CTCCATGCCAACATGTCAGTATGGCTGTATGTTAAAGGAAATACGGTGCAGTGCCTCCATCCCCCTGGCCT  
GCACCTGGCTCTGATGGGAGGACCTGTGATGATGTTGAATGTGCTACAGGAAGGCCCTCTGCCCTAGATT  
TAGGCATATGTCACACTTTGGGAGCTACATCTGCAAGTGTCATAAAGGCTTCGATCTCATGTATATTGGAGG  
CAAATATCAATGTATGACATAGACGAAATGTCACTTGGTCAGTATCAGTGCAAGCAGCTTGCTGATGTTATAA  
CGTACGTGGTCTACAAGTCAAATGTAAGAAGGATACCGGGTGTGGACTGACTTGTGTATATCCAAA  
AGTTATGATTGAAACCTTCAGGTCAAATTGTCACAAAGGGAAATGGTACCATTTAAAGGGTACACAGGAAA  
TAATAATTGGATTCTGATGTTGGAGTACTTGGTGGCTCCGAAGACACCATATATTCTCTATCATACCAA  
CAGGCCTACTCTAAGCCAACAACAAGACCTACACCAAAAGCCAACACCAATTCTACTCCACACCACACC  
CCTGCCAACAGAGCTCGAACACCTCTACCACCTACAACCCAGAAAGGCCAACACCAGGACTGACAACATAGC  
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACGCCCTAGAAACCCAGGAG  
AGATGTGTCAGTGTCTGGTACACAGTTGTAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCACTGGGAAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGGCCAGG  
GGGAAAAGCTGACGCTGGTGTACCTCTCGGCCCTCATGCATTAGGGACTGTGCTGTCAATTAGGCA  
CAAGGTGACGGGCTGCACTCTGCACACTCCAGGTGTTGTGAGAAAACAGGTGCCACGGAGCAGCCCTGTG  
GGGAAGAAAATGGTGGCATGGCTGGAGGCAAACACAGATCACCTTGCGAGGGCTGACATCAAGAGCGAATCACA  
AAGAT**G**ATTAAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACGGGATTATTGAGCCTGGAGAAG  
AGAAGACTGAGGGCAAAACATTGATGGTTTCAGTAAAGATGGTCTAGACTAGAGTAAAGGAGGAGGAGGAG  
TTCTCCATATGCACTAAGAATAGAACAGAGAAACTGGCTTAGACTAGAGTAAAGGAGGAGGAGGAG  
GGCCATTGTTAGAATACTCTATTAAGGAAAGTGTGAAAATTCTCAGTATCTCTCTCTTTCTAAAAAATTAGA  
AAAAAATTGCTCTATTAAAGATGGTAAAGATGGTCTTACCAAGGAAAAGTAACAAATTATAGAATTTCACAA  
AGATTTTGATCCTACTAGTAGTATGCAAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
CATTCCCTCTGACCTCTAATGGAGAGGGATTGAAAGGGAAAGGCCACCAATGCTGAGCTCACTGAAATA  
TCTCTCCCTTATGGCAATCTAGCAGTATTAAGAAAAAGGAAACTATTTATTCACCATGAGAGTATGATGGAC  
AGATATTCTAGTATCTCAGTAATGTCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC  
TTTCATTGTTCAATGGATGATGTTCAAGATTTTTTTAAGAGATCCTCTCAAGGAACACAGTTAGAGAG  
ATTTCATGGGTGCAATTCTCTCTGCTCTGTTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCCTGCC  
ACACCGCAGACCTTCTCACCTCATCAGTATGATTGACTTCTTATCAATTGGACTCTCCAGGGTCCAC  
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTTCTGTCATTAAACCTGGTAAAGGCAGGGCTGG  
AGGGGGAAAATAAAATCATTAAGCCTTGTGACTAACGGCAGAATATGGCTGTAGATCCATTAAATGGTTCAATT  
TCCTTATGGTCAATATAACTGCACAGCTGAAGATGAAAGGGAAAATAAAATGAAATTTACTTTGATGCCAA  
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTAAATGTTT  
CTAAAATAAAAATGTTAGTGGTTTCCAAATGGCCTAATAAAAACAAATTATTTGTAATAAAACACTGTTAGTAAT

## **FIGURE 110**

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCP  
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPC KRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDRTCDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPA AASTPPGGITVDN  
RVQTDPQKPRGDVF SVLVHSCNF DHLGCGWIREKDNDLHWEPIRD PAGGQYLTVSAAKAPGG  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGLQVFVRKHGAALWGRNGGHGWQTQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## **FIGURE 111**

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTCGCCCTTAGATTGTGA  
**AATGGCTCAAGGTCTCACAACTTCCCTTGCAACAGGTGCTGCTCGGGGCTGA**  
AGGTGACAGTGCATCACACACTGTCCATGGCGTCAAGAGGTCAAGGCCCTACCTACCCGTC  
CACTATGGCTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA  
ACAATGCCAAATACCTACTGGGCTCTGTGAATAAGTCTGTGGTCCTGACTTGAATACC  
AACACAAGTTCACCATGATGCCACCCAATGCATCTGCTTATCAACCCACTGCAGTCCCT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGAAATGGAACTCTATGCCAGTCA  
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCACTCCTCC  
CTGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGGACTCGG  
CTAGCTTACCAATGGCTAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTT  
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT  
GCCTGGTGAGGAACCTGTCAGTGAAATGAAAGTGATATCATTATGCCATCATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT  
ATATCCATGTGCTCTCTTCTATGGAAAAAATATCAACCCATAAAAGTTAAAAACAGAA  
ACTAGAACGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATGAATTGTTCTCAGATGTTCTGGTGTGTTCCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGATCGGGGCAAGATTGCACAGTACAGT  
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGT**TGA**ACTTCTATGG  
GCTAACAGTACATTGAGTGAAGAAACATTGAAAGAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCTTTACA  
TGCAGAACAGGATTATGCAAATTGAACTGCAGGTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGTTCTCATAAGTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCACCTACAAA  
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTGTATTAAATTATTAGTG  
TTAAGAATGCTAAATTATGTTCAATTCTATCTGTTATTGTACAA  
CAAAGTAATAAGGATGGTTGTCAAAAAACAAACTATGCCTCTCTTTCAATCACC  
AGTAGTATTTGAGAAGACTTGTGAACACTTAAGGAATGACTATTAAAGTCTTATTGTTA  
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGCTTTAAAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ  
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGCGAAATGGCGCCCTCCGGGAGTCTTGCAGTCAGTCCCCTGGCAGTCCTGGTGTGTT  
GCTTGCGGTGCTCCCTGGACGCACGGGGCGGGAGCAACGTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCGTGGTGCCTGCT  
TGTCAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC  
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAACTTATAAGTGTAAAGAGTGGAAAGAGTATTGAGGCCGTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCAGTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTATTGAAAGACCTGGATTGCCAGTGTGGGATCATATACT  
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC  
AGATTGCCTTGTCCTCAAAAAGGCCAGACCACAGCCATAACCCATAACCCCTCAAAAAAAAT  
TATTATCAGAATCTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCCGATGAAGAA  
GATGTTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAACATGC  
CATAAGACAAACGCTCTGGGTCCATCATTGCCACAGATAATCCTAGTTAAATTTATAG  
TTATCTTAATATTATGATTTGATAAAAACAGAAAGATTGATCATTTGTTGGTTGAAGTG  
AACTGTGACTTTTGAAATATTGCAGGGTTCACTAGTCTAGATTGTCATTAATTGAAGAGTCTA  
CATTCAGAACATAAAAGCACTAGGTATACAGTTGAAATATGATTAAAGCACAGTATGATG  
GTTTTAAATAGTTCTCTAATTGGAAAAATCGGCCAACGAAATAAGATTATGTATATTGT  
TTAATAATAAACCTATTCAAGTCTGAGTTGAAAAATTACATTCCCAAGTATTGCAATTAT  
TGAGGTATTAAAGAAGATTATTAGAGAAAAATATTCTCATTTGATATAATTGCTCTG  
TTTCACTGTGTGAAAAAAAGAAGATATTCCATAATGGGAAGTTGCCATTGTCTCAAG  
AAATGTGTATTCACTGACAATTCTGGTCTTTAGAGGTATTCCAAAATTCCCTTGT  
ATTTTTAGGTTATGCAACTAATAAAACTACCTTACATTAATTACAGTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTAAGTTCATGGTATTCTCTGATTC  
CAACAAAGTTGATTTCTCTGTATTTCTTACTTACTATGGGTACATTTTTATT  
CAAATTGGATGATAATTCTGGAAACATTGTTATGTTTAGTAAACAGTATTGTTGTT  
GTTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGTAATTAAAATT  
TTGGCCACTTTTCAGATTTCATCATTCTGCTGAACCTCAACTGAAATTGTTTTT  
TTTCCTTTGGATGTGAAGGTGAACATTCTGATTTGTCATGTGAAAAAGCCTGGTA  
TTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCAATTCTACTCAGGAAAAG  
CATCTTCTTGATATGCTTAATGTATTGTCCTCATATACAGAAAGTTCTAATTGAT  
TTTACAGTCTGTAATGCTGATGTTAAAATAACATTTTATATTGTTAAAAGACAA  
ACTTCATATTATCCTGTTCTTCTGACTGGTAATTGTCGGGATTCACAGGAAAAA  
GTCAGTAGGATGGAACATTAGTGTATTTCATCCTTAAAGAGCTAGAACATAGTTT  
CACCTTAAAGAAGGGGAAATCATAAATACAATGAATCAACTGACCATTACGTAGAC  
AATTTCGTAATACAAGTTCTTAAAGCCCTCTCTTAAAGAATTAAAATTGTCACCA  
TATCGTAATACAAGTTCTTAAAGCCCTCTCTTAAAGAATTAAAATTGTCACCA  
AAAGAGTTGGATGTGTAATTGTCAGGAAATATCCTAAGCACAAAATAACCT  
TTCTAACCACTCATTAAAGCTGAAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCGAGTGTCCAGCTGGGAGACCGTATAATTCTTAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG  
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCTCTGTGACC**ATGAAACTCTGGGTGTCTGC**  
**ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGTCAGGCCAATTCTCACCTTATTG**  
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGCTAAACACAGACTGGCCTGGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA  
GGTTTATGCCAACCTCTGTGCAGCGGCAGTTCTCCCCACTGATGAGGAGCAGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGTGATGCCGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCCGCCGCTGCTC  
TCCCTGACCCAAGCCACGAACGAGCTGGAGGGATCTGGGTACTTGTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGTGCTGGG  
GAGGGTGTCAAACGTACACCCCCTAGACAGAAGAGGCTTTCTGTAGGTACCAACATGGCA  
CAGGGCCCCACAGCTGCTCATTGCCCTCAAGAGGAGGACGAGTGGGACAGCCCGACA  
TCGTCAGGTACTACGATGTCATGTCATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGACGAGCCACCGTTGATCCAAAGACAGGAGTCTCACTGTGCCAGCTA  
CCGGTTTCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCACCTTTGACAGCGG  
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG  
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTGCGGAGCGGGAAAGGTGACTACCGAACAGACATGCTGCC  
TGTGCTTGTGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACT**TGAC**ATCCTTCTGTCTTCCCTTGGTC  
CTTCAGCCCAGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGGAGAAATGAATGTTGTCAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT  
TGACTGAAGTCCCAGCCCTCATTAGCCTGTGCCATCCCTGGCCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCACTGAACCAAAGTTCTGATACCTTGTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGCTTACCAAGAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSHVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIWSA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGYYHTV  
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPHSERAGGNLR  
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDPYLPERDVYESLCRGEGVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYVDVMSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## **FIGURE 117**

GCAGTATTGAGTTTACTTCCTCCTTTAGTGGAAAGACAGACCATAATCCCAGTGTGAGTGAATTGATTGT  
TTCATTATTACCGTTTGGCTGGGGTAGTTCGGACACCTTCAGTTGAAGAGCAGGCCAGAAGGGAGTTGTGA  
AGACAGGACAATCTCTGGGATGCTGGCCTTGGAAAGCCAGCGGGCCTGCTCTGCTTTGGCCTCATGACCC  
CAGGTTCTCTGGTAAAGCTACTACTGGCCTGGGCCATCAATCATTGATCCTTGAGGCTGTGCC  
CCTGGGCACCCACCTGGCAGGGCTACCACCATTGCACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC  
CCCTCATCTTAGGGCTGCTCTGGGCTGAGCCTCCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG  
ATCCCTGTGTCGAGGCTGTAGGGAGCGAGGAGGGCACAGAACATCCAGATTGAGAGCTGGCTAGACCAAAGTG  
ATGAAGACTTCAACCCCCGATTGTCCCCACTACAGGGACCCAAACAAGCCCTACAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCGAGCTACACTGTCCA  
CTTGGCCGTGGCTGTGAACCGTACGGTGGCCATCACTTCCCTCGGTTACTCTACTTCACTGGCAGGGGGGG  
CCCGGGCTCCAGCAGGGATGCAAGGTGGCTCATGGGATGAGCGGCCCGCCTGGCTCATGTCAGAGACCCCTGC  
GCCACCTTCACACACACTTGGGCCACTACGACTGGTCTCATCATGCAAGGATGACACATATGTCAGGCC  
CCCGCCTGGCAGCCCCCTGCTGCCACCTCAGCATCAACCAAGACTGTACTTAGGCCGGCAGAGGAGTTCATGG  
GCGCAGGCAGCAGGCCGGTACTGTCTGGGGCTTGGCTACCTGTTGTCAGGAGTCTCTGCTTCGTGCTGC  
GCCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGCCTGACAGTGGCTTGGACGCTGCCTCATGG  
ACTCTCTGGCGTGGCTGTCTCACAGCACCCAGGGCAGCAGTATGCTCATTTGAACTGGCCAAAATAGGG  
ACCCCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTCGCCGTGACCTGTCTCCGAAGGTACCCCTCATGG  
ACCGGCTCCACAAACGCTTCAGCGCTTGGAGTTGGAGCGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA  
TCCGGAACCTGACCGTGTGACCCCCGAAGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCTTCA  
CACCACACTCTGCTTGGAGGTGCTGGCTGGACTACTTCAACAGAGCAGCACACCTCTCCTGTCAGATGGGG  
CTCCCAAGTGCCACTACAGGGGCTAGCAGGGGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
ATCGGCCTATCAGCCCCGCTCGCTTCCAGAACAGCAGGACTGCTCAACGGCTATCGGCCTTCGACCCAGCAC  
GGGGCATGGAGTACACCTGGACCTGTTGGAATGTGTGACACAGCGTGGCACCAGGGCCTGGCTCGCA  
GGGTCACTGCTGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC  
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAAGCCCCGGCTTCTCGAGGCGTTGCAAGCAATGTC  
TGGAGCCACGAGAACATGCATTGCTCACCTGTTGCTACGGGCCACGAGAAGGTGGCGTGGAGCTCCAG  
ACCCATTCTTGGGGTAGGGCTGCAGCAGCGAGTTAGAGCGACGGTACCCCTGGGACGAGGCTGGCTGGCTCG  
CTGTGCGAGCAGAGGCCCTTCCCAGGTGCGACTCATGGACGTTGCTCGAAGAACGACCCCTGTTGACACTCTCT  
TCTTCCCTTACACCCGTGTTGACAAGGCCCTGGGCCCCAAGTCTCAACCGCTGTGCCATGAAATGCCATCTGGCT  
GGCAGGGCTTCTTCCAGTCCAGGACTTCAATCTGCCCTGTCACACAGAGTACCCCCCAGGGGG  
CGGGGGCTGGCCCTGACCCCCCCTCCCTGGTGTGACCCCTCCGGGGGGCTCTATAGGGGGGAGATTG  
ACCGGCAGGCTTCTGGGAGGGCTGCTTACAACCGCTGACTACCTGGCGCCCGAGCCGGTGGCAGGTGAAC  
TGGCAGGCCAGGAAGGGAGGAAGGCCCTGGAGGGCTGGAGGGTGTGGATGTTTCTCGGTTCTCAGGGCTCC  
ACCTCTTCTGGGCCGTAGAGCAGGGCTGGTGCAGAAGTCTCCCTGCGAGACTGCAGCCCACGCTCAGTGAA  
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGGCCGTGCCCCAGCTGGCTATGGCTCTTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCCCGCTGGGGCCCTAACCTCATACCTTCTGGTGTGCCCCAGCC  
CCAGGAAGGGCAAGGAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA  
ACATGTCCTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPD  
SRARLDQSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLA  
VAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSQHDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTP  
HSRFEVLGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPR  
LRFQKQRLLNGYR RFDPARGMETYLDLLLEC  
VTQRGHRRALARRVSLRPLSRVEILPMPYVTEATRVQLVLP  
LLLVAEAAAAPAFLEAFAA  
NVLEPREHALLTLLVYGPREGGRGAPDPFLGVKA  
AAAELERRYPG TRLAWLAVRAEAPSQVRLMDVVSKHPVDTLFFLTTVWTRPGPEV  
LNRCRMNAISGWQAFFP VHFQEFPALSPQRSPGPPGAGPDPPSPGADPSRGAPI  
GGRFDRQASAEGCFYNADYLAA RARLAGELAGQEEE  
EALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR CRLSNLEGLG  
GRAQLAMALFEQE  
QANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 119**

CGGAGTGGTGCACGTGAGAGGAAACCGTGCACGGCTGCCTTCCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG  
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTGAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTTGTAAAACC  
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG  
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC  
GTTCTCCTTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTGTTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGTATGGGTATACGCCCTAGGGCATTGGCATATTTCAAT  
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTAGTAGTAACATACATATCCAA  
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGAAATG  
TGGTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTAT  
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTTGCTGATTGGTT  
AAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTAGCTGTGTTCCCTTACTTCTAATACTGATTATGTTCT  
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAATGTACAACAGCAACTAAAGAAA  
ATTAAAGTGAAGTTGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

## **FIGURE 122**

MNSSKSSETQCTERGCFSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGS

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## FIGURE 123

GGGACTACAAGCCGCCCGCTGCCGCTGGCCCTCAGCAACCCCTCACATGGCGCTGAGGC GGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGACTCTTCCGTGCTGCTTTCAAGGGCTGCCTGATAAGGGCTGTAATC  
TCAAATCCAGCAATCGAACCCAGTGTACAGGAATTGAAAGTGTGGAACTGTCTTGCACTCATTACGGATTGCG  
AGACAAGTGACCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTTTTGACAACAAAA  
TTCAGGGAGACTGGCGGTGCGTGCAGAAACTGGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGTGCGTGCAGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGCACCCCTGTCTGTAGAGTGGCGAAGGCTGTACCGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGGAGGGCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT  
CCAGAGCCAATCCCAGATTGCAATTCTTCACTTAAACTCTGAAACAGGCACTTGGTGTTCAGTGC  
TTCACAAGGACGACTCTGGCAGTACTACTGCATTGCTTCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGAATTATTGGGGGTTCTGGTTGCTTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAAGATGGAGTTAATCATCCGCACTGACGAGGAGGGCACTTCAGACACAAAGTCATCGTTG  
TGATCTGAACCCCGGGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTAGAAGCTTTCTGTTGGCAAAGTTGACCA  
CTACTCTTCACTCTAACAAAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTACTGAGTTGGGCTTAATCTGTTCTGGCCTGATTCCGCATGAGTATTAGG  
GTGATCTAAAGAGTTGCTCACGTAACGCCGTGCTGGGCTGTGAAGGCCAGCATGTTACCACTGGTCGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGCGGGAAACCCA  
GAAAAGGCTTCTACACAGCAGCCTACTTCATCGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC  
TGATCGGTGTTGAGTGTCCATTGTGGAGAAGCTTTGGATCAGCATTGTAACAAACACAAATCAGGAAG  
GTAAATTGGGTGCGGAAGAGGGATCTGCGTGGAGAACCCCTGCTTGTCAACAGGGTGTCAAGGATTTAAGGAAA  
ACCTTCGCTTAAAGCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTATTAAATAAATTT  
TACATCTAAATTGGTCAAGGATGTATTGTGATTATTGAAAGAAAATTCTATTAAACTGTAATATATTGT  
CATACAATGTTAAATAACCTATTAAAGGCTAACCTTAAGGTAGAAGTCCAAGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAAAGAGTATTAAACCCAGGAATCCTCTCATGGAAAGTTACTGTGATGTTCTTTCT  
CACACAAGTTTAGCCTTTCAAGGAACTCATACTGTCTACACATCAGACCATAGTGTCTAGGAAACCTT  
TAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCTCATCTTCAAAAGAACCTCTCAGGTTAGCTTGAAC  
GCCTCTCCTGAGATGACTAGGACAGTGTACCCAGAGGCCACCCAGAACGCCCTCAGATGTACATACAGATG  
CCAGTCAGCTCCTGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCCTCGCTGCTGCCAGGAGGCCCT  
GCCATCTGGGCCCTGGCAGTGGCTGTGCTCCAGTGAAGTTACTCACGTGCCCTTGCTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTGGCTCTGTAACAGACCTCT  
TTTGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTAAAGGTTAAAGTTGTTAAATTATTGTT  
AAGATTGCTAAGGCCAAGGCAATTGCGAAATCAAGTGTCAAGTACAATAACATTAAAGAAAATGGAT  
CCCACTGTTCTCTTGCACAGAGAACGCCACAGGCTCTGCGCATTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAGGCCCTGGCGGGGAGGAAAG  
TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTTCATCCGCCGAGACACTGCTCCCATT  
TGTGGGGGACATTAGCAACATCACTCAGAACGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCCTGGA  
GAATGGCTCTCACTACTCACCTGTCTTCAGCTTCCAGTGTCTTGGTTTTAATACTTTGACAGCTTTTTT  
AATTGCAATCATGAGACTGTGTTGACTTTTTAGTTATGTAAGAACACTTGCCTGAGGCCCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCCTCTGGTCTGCTGCATGGCATTGGATGCTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGTAGAGAGGGATGGCTCCCAACCTCAGCGTTGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTCATAGTGTAGGGTAGCCTATTGCCCCCTCTTCTTACACCTAAACCTCTACACTAGTGCCA  
TGGGAACCAAGGCTGAAAAAGTAGAGAGAACGTAAGTAGAGTCTGGGAAGTAGCTGCCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTTACTAACACACCGTAATTGGCATTGTTAAC  
CTCATTATAAAAGCTTCAAAAAACCCA

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAHPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGLVFTAVHKDDSGQYYCIA SNDAGSARCEEQEMEVYDLDNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267